

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:43 ; Search time 6808.06 Seconds
(without alignments)
16857.498 Million cell updates/sec

Title: US-10-782-141-2

Perfect score: 2019
Sequence: 1 gggaaaaatacgaatcctta.....atagttattatcaatlaa 2019

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	2019	6	CQ868325 Sequence
2	2019	100.0	2145	6	CQ868324 Sequence
3	2010	99.6	2010	6	CQ868327 Sequence
4	949.2	47.0	3746	1	AB074414 Sequence
5	803.6	39.8	4100	1	AB112346 Sequence
6	747.2	37.0	2082	6	CQ868312 Sequence
7	747.2	37.0	5980	6	CQ868311 Sequence
8	739.8	36.6	2073	6	CQ868314 Sequence
9	214	10.6	3931	1	AB161456 Sequence
10	197.2	9.8	2028	1	BTU88189 Sequence
11	180.6	8.9	2024	1	BTU88188 Sequence
12	172.4	8.5	3468	6	AR143378 Sequence
13	172.4	8.5	3468	6	AR567184 Sequence
14	172.4	8.5	3471	6	BD062618 Sequence
15	172.4	8.5	3471	6	BD128371 Toxin ac
16	172.4	8.5	3471	6	AR205863 Sequence
17	172.4	8.5	3471	6	AR339971 Sequence
18	172.4	8.5	3471	6	AR559861 Sequence

19	172.4	8.5	3726	6	AR143379 Sequence
20	172.4	8.5	3726	6	AR567185 Sequence
21	172.4	8.5	3837	1	BTCRY1GL
22	172.4	8.5	12579	1	BTCRY1
23	162.8	8.1	2407	6	AR359378 Sequence
24	162.8	8.1	2407	6	AX098659 Sequence
25	147.4	7.3	3668	1	AB185105 Sequence
26	133.6	6.6	4391	1	BTU8665
27	119.8	5.9	1959	6	AR359366 Sequence
28	119.8	5.9	1959	6	AX098635 Sequence
29	118.4	5.9	1986	6	CQ868322 Sequence
30	118.4	5.9	2016	6	CQ868320 Sequence
31	118.4	5.9	2049	6	CQ868318 Sequence
32	118.2	5.9	3666	1	AY138457 Sequence
33	118.2	5.9	3842	1	BTMCXYIBC
34	118.2	5.9	3934	1	BACCRYIE
35	118.2	5.9	3934	6	AR068828 Sequence
36	118.2	5.9	3934	6	I38760
37	118.2	5.9	3934	6	I70138
38	118.2	5.9	8306	1	BTU07026
39	117.6	5.8	1806	6	CQ868303 Sequence
40	117.6	5.8	1890	6	CQ868301 Sequence
41	117.6	5.8	2190	6	CQ868300 Sequence
42	116.8	5.8	2549	1	AY570734 Sequence
43	116.8	5.8	3684	1	AF077326 Sequence
44	116.8	5.8	3684	6	I90319
45	116.8	5.8	3684	6	AR359400 Sequence

ALIGNMENTS

RESULT 1
CQ868325
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
cereus group.
REFERENCE
1
Carozzi N., Hargies T., Koziel M.G., Duck N.B. and Carr B.
TITLE
JOURNAL
Patent: WO 2004/074462-A 26 02-SEP-2004;
Athenix Corporation (US)
FEATURES
source
1. 2019
/organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1428"
1. 2019
/note="unnamed protein product"
/codon_start=1
/transl_table=1
/protein_id="CAH33957.1"
/db_xref="GI:51998372"
/translation="MKNNSTQNTNTEYELIDSGPNNNTNNSRYPKADNIPINIDA
CQRPQDTSVSDIVTIGTYLIFLLEPGIGIVIFSLINKLIPSSQSVAAUSI
CDVSIIRKEDVESVSDVADPEGEHTYVODYLLALDMLDKSNPKQADVAQF
QAREEDFTKLGLSLRQRAEILPLTYQANVHLLRLADAYKKEWGLVCPPLP
GSGRTDNERLAKKIKERYNLCVGNKGLDOIRQGTSAEWSKPKREWTFLAV
DIALPIYDFEYKPLATSVLELREIYTPDVGSGNCGMERFNSVANGNTRGK
LYTWLQALIIYSINILQGLYSGKGTREHYEDFTKNGAFAQMSGTTGNPNITFG
NDFIKTISLARMQPEVGYISLPHLVSRAEPFTTLWFLTEVSSGSGSTESLV
PGINKLPSPSRNYSRLSNACVQNETSRVNVFWGTHSMKKDNKIYDPKTIQIPAV
KAFALPAGTVAGVYTAGPGYGVVTLPYQASIKIKLTSAPTKNRRVRLRYVAG
GPEPFRVERMSPSVSNANFSRATGSGSPDYDTLVTFPNQSGVEIITLQNSGYHL
IYDKVEFIFIDIQIEKTCQPEGDICREGVQSLTKKEIVNSLFIN"

ORIGIN

Query Match		100.0%;	Score 2019;	DB 6;	Length 2019;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2019;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GTGAAAATATGTAATTTCTTATCAAAAATACAAATGAATATGAAATTCGTAGTGTCCCG	60		
DB	1	GTGAAAATATGTAATTTCTTATCAAAAATACAAATGAATATGAAATTCGTAGTGTCCCG	60		
QY	61	AATAACAAATATGTCACAAAGATATCCTTTTGCAAGATCCCAATATATTTCTATTT	120		
DB	61	AATAACAAATATGTCACAAAGATATCCTTTTGCAAGATCCCAATATATTTCTATTT	120		
QY	121	AACCTGACGCTGTGACGGAAGGACATGSCAGATATCGTGGAATCAGTCTCGATATA	180		
DB	121	AACCTGACGCTGTGACGGAAGGACATGSCAGATATCGTGGAATCAGTCTCGATATA	180		
QY	181	GTACATTTGGGACATACCTTATACAAATCTTGCTAGAACCCGGTATAGGTGAATTCCT	240		
DB	181	GTACATTTGGGACATACCTTATACAAATCTTGCTAGAACCCGGTATAGGTGAATTCCT	240		
QY	241	GTAAATTTTTCATATATTAACAAATCATTCGCTCTTCTGTCATCTGTGAGCAGACTT	300		
DB	241	GTAAATTTTTCATATATTAACAAATCATTCGCTCTTCTGTCATCTGTGAGCAGACTT	300		
QY	301	TCTATATGTAATTTAGTATCTATATTCGTAAGAGGTAGACGAGACGCTTAAAGTGAC	360		
DB	301	TCTATATGTAATTTAGTATCTATATTCGTAAGAGGTAGACGAGACGCTTAAAGTGAC	360		
QY	361	GGGGTTGACAGATTTTGAAGGTGAATGACCTGCTTATCAGATTAATTAATCTTCAATTCCT	420		
DB	361	GGGGTTGACAGATTTTGAAGGTGAATGACCTGCTTATCAGATTAATTAATCTTCAATTCCT	420		
QY	421	GAGATTTGGCTTACAGATTAATCAAAATCCTAATAAAATCTTGCTACAGATTAACAGTTC	480		
DB	421	GAGATTTGGCTTACAGATTAATCAAAATCCTAATAAAATCTTGCTACAGATTAACAGTTC	480		
QY	481	CAAGCAAGGAGAAAGATTTCACTTAACTTTTAGCAGGGTCATTTATCAAGACAGAAAGCT	540		
DB	481	CAAGCAAGGAGAAAGATTTCACTTAACTTTTAGCAGGGTCATTTATCAAGACAGAAAGCT	540		
QY	541	GAATATTTATTTATTCCTTACGTAATGTCAGACCTGCAAAATGCAATTTATTAATTAATGAG	600		
DB	541	GAATATTTATTTATTCCTTACGTAATGTCAGACCTGCAAAATGCAATTTATTAATTAATGAG	600		
QY	601	GACGAGTTAATATTAATAAAGAAATGGGGACTAGTGTCCACCGTTATCCAGGATCA	660		
DB	601	GACGAGTTAATATTAATAAAGAAATGGGGACTAGTGTGTCCACCGTTATCCAGGATCA	660		
QY	661	GGGAGAACTGATTTGTAACGACGGTTTAAAGCCGAAATTAAGATTAATTAATTTATG	720		
DB	661	GGGAGAACTGATTTGTAACGACGGTTTAAAGCCGAAATTAAGATTAATTAATTTATG	720		
QY	721	GTAGGGGTGTATTAACAAAGGTTTATGATCAGATTAAGACAGGCGGTACAAATGCTGAAGTT	780		
DB	721	GTAGGGGTGTATTAACAAAGGTTTATGATCAGATTAAGACAGGCGGTACAAATGCTGAAGTT	780		
QY	781	TGATCGAAATTTAATTAATTTCTAGAGAAATGACCGTTGCGGTATTTGATTAATTTGCT	840		
DB	781	TGATCGAAATTTAATTAATTTCTAGAGAAATGACCGTTGCGGTATTTGATTAATTTGCT	840		
QY	841	ATATTTCAACTATATGATTTTGAATAATATCCATTAGCAACAAGTATAGATTAATGAG	900		
DB	841	ATATTTCAACTATATGATTTTGAATAATATCCATTAGCAACAAGTATAGATTAATGAG	900		
QY	901	GAATTTTATACAGATTCAGTGGGATATTCAGGGGAAATTAATGTTGGGAACGGTTTTT	960		
DB	901	GAATTTTATACAGATTCAGTGGGATATTCAGGGGAAATTAATGTTGGGAACGGTTTTT	960		
QY	961	AGCTTTAATTCGTAAGAAAGAAATGAAACACGGGACCTTGTTAGTACTTGCTTCA	1020		
DB	961	AGCTTTAATTCGTAAGAAAGAAATGAAACACGGGACCTTGTTAGTACTTGCTTCA	1020		
QY	1021	GCTATAGATATATATAGTCAATCTTAATCTTACAGCTTGTTATCTTATGCTGGGG	1080		

DB	1021	GCTATAGATATATATAGTCAATCTTAAATCTTACAGCTTGTTATCTTATGCTGGGG	1080		
QY	1081	GGAACTCGCTATTATGAAGACTTCAACAAAGGTAAAGGTCTTTTCAAGTATGCTGGA	1140		
DB	1081	GGAACTCGCTATTATGAAGACTTCAACAAAGGTAAAGGTCTTTTCAAGTATGCTGGA	1140		
QY	1141	ACTAGAGTAATAATCCAGTAAATTTATTTTGGCAATACCGATATATTTAAATTTAT	1200		
DB	1141	ACTAGAGTAATAATCCAGTAAATTTATTTTGGCAATACCGATATATTTAAATTTAT	1200		
QY	1201	TCATTTAGCTAGATATGCAATGCAACCGTGTGTTGGGTATTCATATCCACGATCTGTT	1260		
DB	1201	TCATTTAGCTAGATATGCAATGCAACCGTGTGTTGGGTATTCATATCCACGATCTGTT	1260		
QY	1261	TCACGTGCAAGATTTTTCGCAACAACCTAAATCTTCTGTATAGGTAAACAGTTCT	1320		
DB	1261	TCACGTGCAAGATTTTTCGCAACAACCTAAATCTTCTGTATAGGTAAACAGTTCT	1320		
QY	1321	GGGTACTCAGACAAATGAAATCTGTTTACAGGATTAATAAGATCTACACCTAGT	1380		
DB	1321	GGGTACTCAGACAAATGAAATCTGTTTACAGGATTAATAAGATCTACACCTAGT	1380		
QY	1381	CGTAACAAATTAATCTCATATGATTAATCAATGCGGATGTTCAAAATGAAACCTCAGA	1440		
DB	1381	CGTAACAAATTAATCTCATATGATTAATCAATGCGGATGTTCAAAATGAAACCTCAGA	1440		
QY	1441	GTTAAAGTATTTGGTGGACACATACAGATTAAGAAATATATCAATTTATTCAGAT	1500		
DB	1441	GTTAAAGTATTTGGTGGACACATACAGATTAAGAAATATATCAATTTATTCAGAT	1500		
QY	1501	AAAAATTAAGCAATTCCTGACATAAAGCTTTGCTTACAGAGGTATACAGATATGCA	1560		
DB	1501	AAAAATTAAGCAATTCCTGACATAAAGCTTTGCTTACAGAGGTATACAGATATGCA	1560		
QY	1561	GGAGGTACGTACAGCTGGGCTGCTGTTATACAGAGGAGATGTAGTACGTTACCTTAT	1620		
DB	1561	GGAGGTACGTACAGCTGGGCTGCTGTTATACAGAGGAGATGTAGTACGTTACCTTAT	1620		
QY	1621	CAAGCAAGTTTAAATAATACGTTTAACTTGTGACCCACGAATTAATTAATCCGTGTAGA	1680		
DB	1621	CAAGCAAGTTTAAATAATACGTTTAACTTGTGACCCACGAATTAATTAATCCGTGTAGA	1680		
QY	1681	CTTGCTACGAGGTGAGGACCTGCTCGCTTACAGATTAAGAAATGTCGCAAGTTCT	1740		
DB	1681	CTTGCTACGAGGTGAGGACCTGCTCGCTTACAGATTAAGAAATGTCGCAAGTTCT	1740		
QY	1741	GTTTCAATGCTAATTTTCTGTCAGCTACAGGTGCTATATGTTCAATTTGATTAATG	1800		
DB	1741	GTTTCAATGCTAATTTTCTGTCAGCTACAGGTGCTATATGTTCAATTTGATTAATG	1800		
QY	1801	GACACCTTATGTTACTATTAATCAATCAGGTGTTGAAATTAATTAACAAATCTATCT	1860		
DB	1801	GACACCTTATGTTACTATTAATCAATCAGGTGTTGAAATTAATTAACAAATCTATCT	1860		
QY	1861	GGTACCACTTATTTGTTGCAAAAGTCCAAATTTATCCCAATTTGACATCCAAATTTGAAA	1920		
DB	1861	GGTACCACTTATTTGTTGCAAAAGTCCAAATTTATCCCAATTTGACATCCAAATTTGAAA	1920		
QY	1921	TGTACGAATTTCAATTTGCAAGAGACATATGTAGATGTGAAGGATCAATCTTTGAA	1980		
DB	1921	TGTACGAATTTCAATTTGCAAGAGACATATGTAGATGTGAAGGATCAATCTTTGAA	1980		
QY	1981	ACAAAAAAGAAATGTAAATAGTTTATTTATCAATTA	2019		
DB	1981	ACAAAAAAGAAATGTAAATAGTTTATTTATCAATTA	2019		
RESULT 2					
Q0868324 2145 bp DNA linear PAT 13-SBP-2004					
LOCUS Q0868324					
DEFINITION Sequence 25 from Patent WO2004074462.					
ACCESSION Q0868324					

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
CQ668324.1	GI:51998370	Bacillus thuringiensis	Bacillus thuringiensis	Carozzi, N., Hargis, T., Koziel, M. G., Duck, N. B. and Carr, B.	Delta-endotoxin genes and methods for their use	Patent: WO 2004/074462-A 25 02-SEP-2004;	Athenix Corporation (US)	Location/Qualifiers	1. 2145
		Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.							/organism="Bacillus thuringiensis"
									/mol_type="unassigned DNA"
									/db_xref="taxon:1428"
Query Match	100.0%	Score 2019;	DB 6;	Length 2145;					
Best Local Similarity	100.0%	Pred. No. 0;							
Matches 2019;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
1	GTGAAAAATGAATCTTATCAAAATCAAAATGAATGAATCTGGATGCTCCCG	60							
127	GTGAAAAATGAATCTTATCAAAATCAAAATGAATGAATCTGGATGCTCCCG	186							
61	AATAACAAATATGTCAACAGATATCTTTGCAAGATCCAAATATATTTCTATT	120							
187	AATAACAAATATGTCAACAGATATCTTTGCAAGATCCAAATATATTTCTATT	246							
121	AACCTGACGCTTGTCAAGAAAGCCATGCAAGATAGCTGGAAATCACTCGATATA	180							
247	AACCTGACGCTTGTCAAGAAAGCCATGCAAGATAGCTGGAAATCACTCGATATA	306							
181	GTAACTATTTGGAGACATACCTTATTAATTTCTTGCTAGAACCCCGTATAGTGAATTCCT	240							
307	GTAACTATTTGGAGACATACCTTATTAATTTCTTGCTAGAACCCCGTATAGTGAATTCCT	366							
241	GTAAATATTTCAATATTAACAACAACTCATTCGCTTGTGCAATCTGTGGACGACTT	300							
367	GTAAATATTTCAATATTAACAACAACTCATTCGCTTGTGCAATCTGTGGACGACTT	426							
301	TCTATATGTGATTTAGTATCTATAATTTGTGAAGAGGTAGACGAGCGGTATTAAGTAC	360							
427	TCTATATGTGATTTAGTATCTATAATTTGTGAAGAGGTAGACGAGCGGTATTAAGTAC	486							
361	GGGGTTCAGATTTTGGAGGTGAATGACTGTTATCAAGATTAATTTCTCATTAATCTT	420							
487	GGGGTTCAGATTTTGGAGGTGAATGACTGTTATCAAGATTAATTTCTCATTAATCTT	546							
421	GAGATTTGGCTTACGATTAATCAAAATCCTTAATAAACTTGCTGACGTATTAACAGTTT	480							
547	GAGATTTGGCTTACGATTAATCAAAATCCTTAATAAACTTGCTGACGTATTAACAGTTT	606							
481	CAAGCAGCGGAGAAGATTTCACTAACTTTTACGAGGTCATTAATCAAGACAGAACT	540							
607	CAAGCAGCGGAGAAGATTTCACTAACTTTTACGAGGTCATTAATCAAGACAGAACT	666							
541	GAAATATTTATTTATGCTTACGATATGTCAGAGCTGCAATTTGTCATTTATTAATAAG	600							
667	GAAATATTTATTTATGCTTACGATATGTCAGAGCTGCAATTTGTCATTTATTAATAAG	726							
601	GAGCAGTAAATATTAATAAAAGAAATGGGACATAGTGTGCAACGTTTATCAAGGTC	660							
727	GAGCAGTAAATATTAATAAAAGAAATGGGACATAGTGTGCAACGTTTATCAAGGTC	786							
661	GGGAGAACTGATTTGTAACGAGCGTTTAAAGGAAATTAAGATATTAATTAATTTGT	720							
787	GGGAGAACTGATTTGTAACGAGCGTTTAAAGGAAATTAAGATATTAATTAATTTGT	846							
721	GTAAGGTGTATTAACAAGGCTTTAGATCAATTAAGACGCGGGGTCAAGTCTGAAGTT	780							
847	GTAAGGTGTATTAACAAGGCTTTAGATCAATTAAGACGCGGGGTCAAGTCTGAAGTT	906							

QY	781	GGGCGAAATTTAAATATTCGAGAGAAATGCGTTGGCGGATTTGAATTAATGCT	840
Db	907	TGGTCGAAATTTAAATTTTCGAGAGAAATGCGTTGGCGGATTTGAATTAATGCT	966
QY	841	ATATTTCCAACTTAATGATTTTGGAAAAATATCATTTAGCAACAACTGTAGAATTAACTAGG	900
Db	967	ATATTTCCAACTTAATGATTTTGGAAAAATATCATTTAGCAACAACTGTAGAATTAACTAGG	1028
QY	901	GAAATTTATACAGATCCAGTGGGATATTCAGGGGGAAATTAATGGTTGGGAACGGTTT	960
Db	1027	GAAATTTATACAGATCCAGTGGGATATTCAGGGGGAAATTAATGGTTGGGAACGGTTT	1086
QY	961	AGCTTTAATTCGAGTAGAAGCAAAATGAGAACACGGGGACCTGGTTAGTATCTTGGCTTCAA	1028
Db	1087	AGCTTTAATTCGAGTAGAAGCAAAATGAGAACACGGGGACCTGGTTAGTATCTTGGCTTCAA	1146
QY	1081	GGAATCTGCTATTAATGAAAGCTTCCAAAGGGTAAACGGTCTTTTCAAACGTAATCTGGGA	1140
Db	1207	GGAATCTGCTATTAATGAAAGCTTCCAAAGGGTAAACGGTCTTTTCAAACGTAATCTGGGA	1266
QY	1141	ACTACGATATAATACACGTAATATATTTTGGCAATACCGATATATTTTAAATTAAT	1200
Db	1267	ACTACGATATAATACACGTAATATATTTTGGCAATACCGATATATTTTAAATTAAT	1326
QY	1201	TCATTAAGCTAGATATGCAATGCAACCGTTTGGTGGATTAATCCACCGGCATCTTGT	1260
Db	1327	TCATTAAGCTAGATATGCAATGCAACCGTTTGGTGGATTAATCCACCGGCATCTTGT	1386
QY	1261	TCACGTGCAGAAATTTTTCGCAACAACTTAATCTTCCGTATGAGGTAAACAGTCT	1320
Db	1387	TCACGTGCAGAAATTTTTCGCAACAACTTAATCTTCCGTATGAGGTAAACAGTCT	1446
QY	1321	GGGTACTCACAGACAATTTGAATCTGTGTACACAGATATTAATTAAGATCTACACCTAGT	1380
Db	1447	GGGTACTCACAGACAATTTGAATCTGTGTACACAGATATTAATTAAGATCTACACCTAGT	1506
QY	1381	CGTACAAATTAATCTCTCAATATTAATCAAAATGCGCATGTGTCCAAATTGAAACCTCCAGA	1440
Db	1507	CGTACAAATTAATCTCTCAATATTAATCAAAATGCGCATGTGTCCAAATTGAAACCTCCAGA	1566
QY	1441	GTTAACCTATTTGGTTGAGACACATCAAGATATGAAAAAATATCGAATTTATCCAGAT	1500
Db	1567	GTTAACCTATTTGGTTGAGACACATCAAGATATGAAAAAATATCGAATTTATCCAGAT	1626
QY	1501	AAAATTAACGCAATTTCTGCAATTAAGCTTTTGCCCTACACAGCAAGTACAGATATGCA	1560
Db	1627	AAAATTAACGCAATTTCTGCAATTAAGCTTTTGCCCTACACAGCAAGTACAGATATGCA	1686
QY	1561	GGAAGTTAACGTCACAGCTGGGCGCTGGTTATACAGAGAGATGATGATACGTTACCTAT	1620
Db	1687	GGAAGTTAACGTCACAGCTGGGCGCTGGTTATACAGAGAGATGATGATGATACGTTACCTAT	1746
QY	1621	CAAGCAAGTTTAAATAATACGTTTAACTTTCGACCCACGAATAAAAATTAACCGTGTAGA	1680
Db	1747	CAAGCAAGTTTAAATAATACGTTTAACTTTCGACCCACGAATAAAAATTAACCGTGTAGA	1806
QY	1681	CTTTCGCTAACGCGATGAGACCTGGTTCGTTCCGAGTATGAAAGATGTGGCCAAATTC	1740
Db	1807	CTTTCGCTAACGCGATGAGACCTGGTTCGTTCCGAGTATGAAAGATGTGGCCAAATTC	1866
QY	1741	GTTTCAAAATCTAATTTTTCGTCGACGATACAGTGGCTATAGTTCAATTTGATTAATGTG	1800
Db	1867	GTTTCAAAATCTAATTTTTCGTCGACGATACAGTGGCTATAGTTCAATTTGATTAATGTG	1926
QY	1801	GACACCTTAAGTACTACATTTAATCAATCAAGGTGTGAATTAATTAATCAAAATCTATCT	1860
Db	1927	GACACCTTAAGTACTACATTTAATCAATCAAGGTGTGAATTAATTAATCAAAATCTATCT	1986

QY	1861	GGTTACACCTTATGTTGCAAAAGTCGAATTTATCCCAATTGACATCCAAATTTGAAAA	1920
Db	1987	GGTTACACCTTATGTTGCAAAAGTCGAATTTATCCCAATTGACATCCAAATTTGAAAA	2046
QY	1921	TGTACGAAATGTCATTCGAAAGGACATATGTATGTGAAGAGTACATCTTTGAA	1980
Db	2047	TGTACGAAATGTCATTCGAAAGGACATATGTATGTGAAGAGTACATCTTTGAA	2106
QY	1981	ACAAAAAAGAGTTGTAATTAATCTTTATTTATCAATTA	2019
Db	2107	ACAAAAAAGAGTTGTAATTAATCTTTATTTATCAATTA	2145
RESULT 3			
LOCUS	C0868327	2010 bp	DNA linear PAT 13-SEP-2004
DEFINITION	Sequence 28 from Patent WO2004074462.		
ACCESSION	C0868327		
VERSION	C0868327.1	GI:51998373	
KEYWORDS			
SOURCE	Bacillus thuringiensis		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1 Carozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B. Delta-endotoxin genes and methods for their use Patent: WO 2004074462-A 28 02-SEP-2004; Athenix Corporation (US)		
FEATURES	Location/Qualifiers		
source	1..2010		
	/organism="Bacillus thuringiensis"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:1428"		
	1..2010		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_table=1		
	/protein_id="CAH33958.1"		
	/db_xref="GI:51998374"		
	/translation="MNSYQNTNTEYILDGSPPNNTMNSNYPKADNIPINLADCOGRPMDQWESVDIVITGYLIQFLEPGIGLPIVPSIINKLIPSSGQVVALSICDLVSIIRKEDVESLSDGVADEGEMTAYODYLYLDDMLDKENPKLADVVGOPARBEDFTKLIGSLSRKABILLPTVQAAVMHLLLRDVAKYKEMGALVCPPIPSGRITDNEBLLAKIKETNYCYGTGKNGLDIQRNGTSAEYMSKRNKREXTLAVDITLALPITDFEKYPLATISVELTRELITDPVGSNGYMERFSPNSVEANGTRGPGVLTWLOAIDIVSHSINLOGLYLSGWSGTRHYEDFTYNGAFORMSGTSSNNPNTIFGNTDIFKILISLARVAMPFVGYSI.PRLVSRAEFFPTLNTPLLEVNSGYSQTIISLVFGI NKDLPSRTNYSHRLSNACVONETSRVNVFGWTHSMKKDNRIYDKITLOIPAVKAFALPAGTGYAGVYTAGPGYAGDVVTL.PYQASIKIRLTSAPTMKVIRVLRVAGSGGAPVRVRSBSVSVANPNSRPATGYSFDYVDLVLTVPNOSGVEITIIQNLSTGHLIVDKVEFIPIDIQIEKCTKCFEGRDICRCEGVSLTKKEIVNSLFIN"		
ORIGIN			
Query Match	99.6%;	Score 20.0;	DB 6; Length 2010;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2010;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	10	ATGAATTTCTTATCAAAATACAAATGAATATGAATTCGATGTTCCCGGAATTAACACA	69
Db	1	ATGAATTTCTTATCAAAATACAAATGAATATGAATTCGATGTTCCCGGAATTAACACA	60
QY	70	AATATGCAAAAGATATCTTTTGGCAAAGATCCAAATATATTTCTTATTAACCTGGAC	129
Db	61	AATATGCAAAAGATATCTTTTGGCAAAGATCCAAATATATTTCTTATTAACCTGGAC	120
QY	130	GCTTGTACGGAAGGCCATGGAAGATACGTGGGAATCAGTCTCGATATAGTAACTATT	189
Db	121	GCTTGTACGGAAGGCCATGGAAGATACGTGGGAATCAGTCTCGATATAGTAACTATT	180
QY	190	GGGACATACCTTATACAAATCTTGCTAGAAACCCGGTATAGTGAATTCCTGTAAATATT	249
Db	181	GGGACATACCTTATACAAATCTTGCTAGAAACCCGGTATAGTGAATTCCTGTAAATATT	240

QY	250	TCAATATTAACAAACCTGATCCGCTCTTGCTGTCATCTGTGGACGACTTTCTATATGT	309
Db	241	TCAATATTAACAAACCTGATCCGCTCTTGCTGTCATCTGTGGACGACTTTCTATATATGT	300
QY	310	GATTTAGTATCTATTAATTCGTAAAGAGGTAGACGAGACGCTGTATAGTACGCGGTTGCA	369
Db	301	GATTTAGTATCTATTAATTCGTAAAGAGGTAGACGAGACGCTGTATAGTACGCGGTTGCA	360
QY	370	GATTTGAGGGTGAAGATGACGCTTATGCAAGATTATATCTTCAATTAATCTTGAGGATTGG	429
Db	361	GATTTGAGGGTGAAGATGACGCTTATGCAAGATTATATCTTCAATTAATCTTGAGGATTGG	420
QY	430	CTTACAGATTAATTCAAATCTTAAATACTGTGTCGATAGTTAAACATGTCACACGACG	489
Db	421	CTTACAGATTAATTCAAATCTTAAATACTGTGTCGATAGTTAAACATGTCACACGACG	480
QY	490	GAAAGAGATTTCACTAACTTTTACGAGGTCACTATGCAAGACAGAAAGCTGAATATTA	549
Db	481	GAAAGAGATTTCACTAACTTTTACGAGGTCACTATGCAAGACAGAAAGCTGAATATTA	540
QY	550	TTATTGCCCTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTAATTAAGGACGCACTT	609
Db	541	TTATTGCCCTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTAATTAAGGACGCACTT	600
QY	610	AAATATTAATAAAGAAATGGGAGCTAGTGTGTCACCGTGTATTCAGGGTTCAGGAGAACT	669
Db	601	AAATATTAATAAAGAAATGGGAGCTAGTGTGTCACCGTGTATTCAGGGTTCAGGAGAACT	660
QY	670	GATTTGAAACGAGCGGTTAAAGCGAAATTAAGATTAATTAATTAATTTAGTGGTGG	729
Db	661	GATTTGAAACGAGCGGTTAAAGCGAAATTAAGATTAATTAATTAATTTAGTGGTGG	720
QY	730	TATTAACAAGGTTTATGATCATATTAACAGACGCGGTTACAGTCTGAAAGTTTGTGCAAA	789
Db	721	TATTAACAAGGTTTATGATCATATTAACAGACGCGGTTACAGTCTGAAAGTTTGTGCAAA	780
QY	790	TTTAAATTAATTTCTGTAAGAAATGACGTTGGCGGATTTGATTAATTTGATATTTTCCA	849
Db	781	TTTAAATTAATTTCTGTAAGAAATGACGTTGGCGGATTTGATTAATTTGATATTTTCCA	840
QY	850	ACTTATGATTTTGAATAATATCATTTAGCAACAAGTGTAGAGTTAACTAGGAAATTTAT	909
Db	841	ACTTATGATTTTGAATAATATCATTTAGCAACAAGTGTAGAGTTAACTAGGAAATTTAT	900
QY	910	ACAGATCCAGTGGATATTCAGGGGAAATTAATGTTGGGAAACGCTTTTATGCTTTAAT	969
Db	901	ACAGATCCAGTGGATATTCAGGGGAAATTAATGTTGGGAAACGCTTTTATGCTTTAAT	960
QY	970	TGGTATGAAGCAAAATGGAACAAGGGGACCTGGTTTATAGTTACTTGCTTCAACCTATAGAT	1029
Db	961	TGGTATGAAGCAAAATGGAACAAGGGGACCTGGTTTATAGTTACTTGCTTCAACCTATAGAT	1020
QY	1030	ATATATAGTATTTATTAATCTTCAAGCTTGGTATCTTAATGAGGCTGGGGGGAACCTCGT	1089
Db	1021	ATATATAGTATTTATTAATCTTCAAGCTTGGTATCTTAATGAGGCTGGGGGGAACCTCGT	1080
QY	1090	CATTATGAAGACTTCAAAAAGGTTAACGGTGTCTTTTCAACGATGTCTGGAACCTACGAGT	1149
Db	1081	CATTATGAAGACTTCAAAAAGGTTAACGGTGTCTTTTCAACGATGTCTGGAACCTACGAGT	1140
QY	1150	AATTAATCCAGTAAATTAATTTTGGCAATACCGAATATTTAAATTAATTTCAATTAAGT	1209
Db	1141	AATTAATCCAGTAAATTAATTTTGGCAATACCGAATATTTAAATTAATTTCAATTAAGT	1200
QY	1210	AGATATGCAATCAACCGTTGTGAGGTAATCAATCCACGCGCATCTTGTCAAGTGA	1269
Db	1201	AGATATGCAATGCAACCGTTGTGAGGTAATCAATCCACGCGCATCTTGTCAAGTGA	1260
QY	1270	GAAATTTTTCGACAAACCTAAATATCTTCTGTATAGGTAAACAGTTCTGGGTACTCA	1329
Db	1261	GAAATTTTTCGACAAACCTAAATATCTTCTGTATAGGTAAACAGTTCTGGGTACTCA	1320

Oy		1330	GAGCAATTGATCTGTGGTCCAGGGTTTAATAAGATTCACACCGTAGTGTCAAAT	1389
Db		1321	CAGACATTTGAATCTGTGTACAGAGTATTATAAGATCTAACACCTTAGTCACAAT	1386
Oy		1390	TACTCTCAGAATTATCAAATGCGGCATGTGTCCAAAATGAAACCCTCCAGGTTAAGCTA	1449
Db		1381	TACTCTCATAGTTATCAAATGCCGCATGTGTCCAAAATGAAACCCTCCAGGTTAAGCTA	1440
Oy		1450	TTTTGGTTGACACATACACAGTATGAAAAAAGATTAATCGAATTTATCCAGATTAATAACG	1509
Oy		1510	CAAAATTCCTGCAGTAAAGCTTTTGGCCCTACACAGAGGTACAGATATGACGAGGCTTAC	1565
Db		1501	CAAAATTCCTGCAGTAAAGCTTTTGGCCCTACACAGAGGTACAGATATGACGAGGCTTAC	1560
Oy		1570	GTCA CAGCTGGGCGCTGTTATACAGAGAGATGTAGTAAAGCTTATCAAGCAAGT	1629
Db		1561	GTCA CAGCTGGGCGCTGTTATACAGAGAGATGTAGTAAAGCTTATCAAGCAAGT	1620
Oy		1630	TTAAATAATACGTTTAACTTCTTGACCCA CGAATTAATAATCCGTTGAGCTTGCTAC	1689
Db		1621	TTAAATAATACGTTTAACTTCTTGACCCA CGAATTAATAATCCGTTGAGCTTGCTAC	1680
Oy		1690	GCGAGTGAAGAACCTGTGTCGTTCCGATGATGAAAATGTGTGCCAAAGTCTGTTCAAAT	1749
Db		1681	GCGAGTGAAGAACCTGTGTCGTTCCGATGATGAAAATGTGTGCCAAAGTCTGTTCAAAT	1740
Oy		1750	GCTAATTTTTCTCGTCCAGCTACAGAGTGAGTATAGTCAATTTGATATGTGACACCTTA	1809
Db		1741	GCTAATTTTTCTCGTCCAGCTACAGAGTGAGTATAGTCAATTTGATATGTGACACCTTA	1800
Oy		1810	GTTACTACATTTAAATCAATCAGTGTGTGAAATTAATTTATACAAAATCTATCTGTGTTACAC	1869
Db		1801	GTTACTACATTTAAATCAATCAGTGTGTGAAATTAATTTATACAAAATCTATCTGTGTTACAC	1860
Oy		1870	CTTATATGTGGACAAAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGTACGAA	1929
Db		1861	CTTATATGTGGACAAAGTGAATTTATCCCAATTTGACATCCAAATTTGAAAAATGTACGAA	1920
Oy		1930	TGTCAATTCGAAAGGACATATGTATGTATGAAGAGTACANATCCTTGGAAACCAAAAAA	1989
Db		1921	TGTCAATTCGAAAGGACATATGTATGTATGAAGAGTACANATCCTTGGAAACCAAAAAA	1980
Oy		1990	GAGATTGTAATATGTTTATTTATCATTTAA 2019	
Db		1981	GAGATTGTAATATGTTTATTTATCATTTAA 2010	
RESULT 4				
AB074414				
LOCUS		3746 bp	DNA	linear BCT 14-JUN-2003
DEFINITION			Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.	
ACCESSION		AB074414		
VERSION		AB074414.1	GI:16945771	
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS		1	Ito,T., Sahara,K., Asano,S. and Bando,H.	
TITLE			Cloning and Expression of Novel Crystall Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins Unpublished	
JOURNAL		2	(bases 1 to 3746)	
AUTHORS			Ito,T., Sahara,K., Asano,S. and Bando,H.	
TITLE			Direct Submission	
JOURNAL			Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture,Hokkaido University, Kita-5-1you Nishi-9chome, Kita-ku,Sapporo-shi, Hokkaido 060-8589, Japan	

FEATURES
 (E-mail: to-@abs.agr.hokudai.ac.jp, Tel: 81-011-716-2487)

source
 Location/Qualifiers
 1..3746
 /organism="Bacillus thuringiensis serovar aizawai"
 /mol_type="genomic DNA"
 /serovar="aizawai"
 /isolate="Bunt-14"
 /db_xref="taxon:1433"
 1..2002
 /gene="Cry40A"
 <1..2002
 /gene="cry40A"
 /codon_start=2
 /transl_table=1
 /product="putative mosquito cidal toxin"
 /protein_id="BAB72018.1"
 /db_xref="GI:16945772"
 /translation="NSYENKREYEILSSSNNTMPNRYPRANDTHMSVSLSDCGI
 SMDSIESAETITSIGDILFLMEPSLGGSSINTLFSITGLIPIRHHOSVSLSCDLL
 SIKRKEVADSVLSDAICRFLDGKIKNREYLLPLEMLMDGKRPLOKTNSSDIGQVVK
 YFELSERDPNEILGGSLARRNAQIILLPYCASCKQYLIRAVQYEDQMFPFLSAB
 NVSEELISPSNGCDFTGDYERELCKIAEYDCEYVQAGLINOIKQAGADTMAF
 NKPREMTLITVLDIAIFQYIDFKKYLPHVELTREITYDDPGSGTYSMLKYWG
 APTLEANGTRPGELVWLRISGIYGVYVSRYSGGGRHYEDYTGNCFORMSGT
 TSNDRDISFPNSDIFKIESKALIMLVGEINAPRIVRSAPRSESTAFIYLDAGNS
 GLSSMTITPSKLPGINKPEPSRYDRSHLSNAACVGAQNSINIVYGMTHTSMKNLY
 PDKTQIIPYAVAPDISDTGPGVLAGHGKGVNVSIPYSLKILRIIPASTNKNLYV
 RVRTTSNGRLVERVSPSSINSYFELSTGSDGFGVDTLVTFNPGVEIILIQ
 NDRPIVNDKVEPIPNVSTALEYGRKSLKADVNDLRYK"
 2070..3746
 /gene="40orf2"
 2070..3746
 /gene="40orf2"
 /codon_start=1
 /transl_table=1
 /product="Cry40orf2 protein"
 /protein_id="BAB72019.1"
 /db_xref="GI:16945773"
 /translation="MFTNGTKRNTLKIETTYEILDOAISIENSDHSPEKIMLMDDE
 VKRKLTSORNLONGDPDGFYGNMDFPGNNIITIGNSGIPKGNFLPMQSGARDIYGT
 IFPPIYOKIDESKLRKYRVRVPGFGSKDLRIWYRIGKEIDAMNVPNDLAVQC
 PNPSGDSRCRESSQYVSQGPPTPTDIYADRIA CPSSSRKHYMCHDRHPFDHIT
 GELDTNINVGIDIVLFKISNPDGATLGNLVEIEGPIFGSLTHVQKKEKKMKHMEK
 KRMTQADYDPAKQAVDLPFTNEBELHYHLLIYLQILDMYSFPIPYMTGYDAGG
 MNVGYQGNLARIMQAVNLIDARKEVINSGPFGKLGQMHAGRAVQILDGASVLYVS
 NMSGVQGNLHAODHGHVLRVILAKKEGPKGVYTMDCDNGNDELTFKSCEEGYMKR
 TVEYFPESDRVRLEIGTEGTFYVDSIELCMQGYASNNPHNGNRYGQSYNGNYNQN
 TSDVHGGITNNINQNSNMNTNMYTHNDLHSGCTCNQSHNSGCTCSQG"

ORIGIN
 Query Match 47.0%; Score 949.2; DB 1; Length 3746;
 Best Local Similarity 71.4%; Pred. No. 5.3e-173;
 Matches 1466; Conservative 0; Mismatches 458; Indels 88; Gaps 13;
 Db 12
 12 GAATTCCTATCAAAATA CAATGATATGAAATTC TGAATGTTCCCGAATAACACAAA 71
 |||||
 1 GAATTCATATGAATAATAAATGAATATGAATAATGGAATCTTCATCGAATACACAAA 60
 |||||
 72 TATGTCAACAGATATCTCTTTTGCAAGGATCCAAATATATTTCTTATTAACCTGGACGC 131
 |||||
 61 TATCCAAACAGATATCTCTTTTGCAAAATGATCGGATATGCTACTATGCTTTCAATGA 120
 |||||
 132 TTGTGACGGAAGCGCATCGGCAAGATAGTGGGAGATCAGTCTCGGATTTAGTAATATTTGG 191
 |||||
 121 TTGTCAAGGATCTCAATGGAGATGAATTTGGGAATACGCCGAAACGATTAACAGTATTTGG 180
 |||||
 192 GACATACCTTATACAAATCTTGTCTAGAACCCGGTATAGTGAATTCCTGTAAATATTTTC 251
 |||||
 181 GATGATCTTATAGAGTTTGTGATGGAACCTAGTTTGGGTGGAATTAAATACATATTTTC 240
 |||||
 252 AATATATAACAAATCTATTCGCTCTTCTGGTCAATCTGTGACAGCACTTTCTATATGTGA 311
 |||||
 241 AATATATGGAACAAATCTATTCGATATCTCATATCTGTGTCCGCACTTTCTATATGTGA 300
 |||||

QY 312 TTATGATCTATTAATTCGTAAAGAGGAGAGAGCGGTGTTAAGTGAACGGGGT---GC 368
 Db 301 TTATATATCTATTAATTCGTAAAGAGGAGCGCATAGGTTTAAAGTGAATCGATTGGCAG 360
 QY 369 AGATTTTGAAGGTTGAATGA CTGCTTA TCAAGATTTATTTATCTTCAATATCTTGAGATTTG 428
 Db 361 ATTTTGAACGGTTAAATTTGAAGATATTTATCTTCTTATCTTGAGGCTTG 420
 QY 429 GCTTACG-----ATTAATCAATCTTAAATAAATCTTGACGCTAGTTAA 473
 Db 421 GCTTAAAGACGTAAACCACTTCAAAAGACAAATTAATCTGAATTCGCAATTAATTTAA 480
 QY 474 ACAGTTCAAGCAACGGGAGAAATTTCACTAACTTTTACAGGGCTATTATCAAGAC 533
 Db 481 ATATTTGAACTTTCAAGAAAGGATTTTAAATGAATTTCTAGAGATCACTTACAGAGAA 540
 QY 534 GAAAGCTGAAATTAATTAATTTGCC-TACGTATGTCAAGCTGCAAAATGTGCATTTATAC 592
 Db 541 CAATGCTCAAAATATGTTATTTACCTTACTTTTGCAGACCTGCAAATGT-CACTTATTTAT 599
 QY 593 TATTAAGGAGCGAGTTAAATTAATAAAGATGGGAGCTAGTGTGCCACCGTTATTC 652
 Db 600 TATTAAGGAGTGAATTCATTAATGAAGAACAAATGTTCCATTTTGAAGTCAGAGAAATG 659
 QY 653 CAGGTCAGGAGAAC-----TGATTTGTAAGAGC 682
 Db 660 TAAGATCGGAATTAATTCACCTAACAGTGTGTGATTTTACCGGATTTACTATAGAC 719
 QY 683 GGTAAAGCGAAATTAAGAGATTAATAATTTGTAGGAGTGTATTAACAGGGTT 742
 Db 720 GATTAATTAATTAATTAATGACAGATATCCGATTAATGTAATTTGGTATCAGCGGGTT 779
 QY 743 TAATCAGATTAAGACGGGCGGTACAGTGTCTGAAGTTGTGGAATTTAATAATTTTC 802
 Db 780 TAATCAATTAATAACGGCGGAGCAGGTCTGACACTGGCGAAATTTAATAATAATTTTC 839
 QY 803 GTAGAGAAATGACGTGGCGGTATTTGATTAATTTATTTTCCAACTTATGATTTTG 862
 Db 840 GTAGAGAAATGACGTGGCGGTATTTGATTAATTTATTTTCCAACTTATGATTTTC 899
 QY 863 AAAAATATCCATTAAGCAACAGTGTAGATTTAACTAGGAAATTTATACAGATCCAGTGG 922
 Db 900 AGAAATATCCATTAAGCAACAGTGTAGATTTAACTAGGAAATTTATACAGATCCAGTGG 959
 QY 923 GATATTCAGGGGAAATTAATGTTGGACGCTTTTAC-----TTAATTCGGTAG 976
 Db 960 GATATTCATCAGGAATTAATGCTGTAAAGTATGGAACCGGTCTTTAATACGTTAG 1019
 QY 977 AAGCAATGGAACACGGGAGCTGTTAGTTACTTGGCTTCAAGCTATGATATATATA 1036
 Db 1020 AAGCTATGGAACACGGGAGCTGCTTATGTTAGCTTAGAGATTAAGTATATATA 1079
 QY 1037 GTCAATCTATTAATCTTACGCTTGTATCTTGAAGCTGGGAGAACTGTCATTATG 1096
 Db 1080 ATAGATATGT-----TCGAGATATTTTACGGCTGGTGAAGAACTCGCATATATG 1130
 QY 1097 AAGACTTCAAAAGGGTAACGCTGCTTTTGAAGTATCTGGAACCTACAGATTAATATC 1156
 Db 1131 AAGACTTCAAAAGGGTAACGCTGATTTTGAAGTATCTGGAACCTACAGATTAATATC 1190
 QY 1157 CAGCTATATTAATTTTGGCAATACGATATATTAATTAATTTTCAATGCTAGATATG 1216
 Db 1191 TAGTATATTAATTTTCCAAATTCGATATATTTAAATTTGAATCAAAAGCTA---TCA 1247
 QY 1217 CAATGCAACCGTTTGGTATTCATATCCACGGACTCTGTTTCAAGTGAATTTT 1276
 Db 1248 TGAACCTAGTAGAGAGATTAACGCTGACCGGAGTATCGTGTTCACGTCAGAAATTTA 1307
 QY 1277 TTCCGCAACAACATAATCTTCTCTGATAGAGTAAACAGTTCTGGGTA---CTCACAGA 1333
 Db 1308 GTAGATCAACAGCATTAATATACCTGTATGATGACAGTAAATAGTGGCTAAGACAGATCA 1367

QY 1334 CAATGAATCTGTGTTACCGAGTATTAATTAAGATCTATACACCTAGCTGACAAATTACT 1393
 Db 1368 CAATTAATCTATTAATTCAGAGTATTAAGA---ATCCAGAACCTTATTTAGATTAATCT 1424
 QY 1394 CTCAATGATTAATCAAAATGCGGATGTGTTCAAAATGAAAACCTCAGAGTTAAAGTATTTG 1453
 Db 1425 CTCAATGATTAATCAAAATGCGGATGTGTTGAGCTGGCAACAGCAAAATTAATGATATG 1484
 QY 1454 GTTGAACATACATAGTATGAAAAGATTAATCGAATTTATTCAGATTAATAATTAAGCCAA 1513
 Db 1485 GTTGAACATACATAGTATGTAATGTAATTAATTAATTAATTAATTAATTAATTAATTA 1544
 QY 1514 TTCTCTGAGTAAAGCTTTTGGCCCTACAGCAGATACAGATATGACAGAGAGGTTACGTCA 1573
 Db 1545 TACCGCGGTGAAGCTTTTGAATATTCGATATCA-----GGCCAGGTCAAGTCA 1595
 QY 1574 CAGCTGGGCTGTGTTATACAGAGAGATGATGTAACGTTACCTTATCAAGCAAGTTTAA 1633
 Db 1596 TAGCTGACCTGTGATACAGAGAGAAATGTAGTAAGCTTACATATTAATTCACGTTTAA 1655
 QY 1634 AAATAGCTTAACTTCTGACCCAGATTAATAAATTAACGTTTGAAGTCTGCTACGCA 1693
 Db 1656 AAATAGCTTAAATCTGTGATCCAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1715
 QY 1694 GTGAGAACCTGTGCTCGGTCCAGTAGAAGATGGTCCGCAAGTCTGTTCAAAATGCTA 1753
 Db 1716 GTACAGAACATGTAGTATCTAGTATGAAATGATGTCGCGAGTCTATTAATAATAGTT 1775
 QY 1754 ATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTGATTTATGTCACACTTATGTTA 1813
 Db 1776 ATTTTCTTCTCACTACAGGCTCTCGTGATTTCAATTTGGCTATGTGACACCTTATGTTA 1835
 QY 1814 CTACATTAATCAATCAGGTGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1873
 Db 1836 CTACATTAATCAATCAGGTGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1892
 QY 1874 TTGTTGACAAATCGAATTTATCCCAATGTA--CATCCAAATTTGAATAATGTAAGCAATG 1931
 Db 1893 AGCTTGACAAATGATTAATTTATCCAGTCAATTTCAAGGCTTTAGAAATTAAGAGAAAC 1952
 QY 1932 TCAATTCGAAGAGACATATGTAATGTGAAGAGTACAACTCTTGAAAACAAAAGAGA 1991
 Db 1953 AAAGTCTGAAGAAAGGACAAAGATGTAAGTAAATTAATTAATTAATTAATTAATTA 2012
 QY 1992 GATGTAAATAG 2003
 Db 2013 GTACGAAAGTAG 2024

RESULT 5
 AB112346 4100 bp DNA linear BCT 14-JUN-2003
 LOCUS
 DEFINITION
 Bacillus thuringiensis serovar aizawai cry40-like and ORF2 genes
 for putative mosquitoicidal toxin, hypothetical protein, complete
 cds.
 ACCESSION
 AB112346 GI:31745043
 VERSION
 AB112346.1 GI:31745043
 KEYWORDS
 SOURCE
 ORGANISM
 Bacillus thuringiensis serovar aizawai
 Bacillus thuringiensis serovar aizawai
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
 cereus group.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Ito, T., Sahara, K., Amano, S. and Bando, H.
 Cloning and Expression of Novel Crystal Protein Genes from *Bacillus*
thuringiensis subsp. *aizawai* Encoding Mosquitoicidal Proteins
 Unpublished
 2 (bases 1 to 4100)
 Ito, T., Sahara, K., Amano, S. and Bando, H.
 Direct Submission
 Submitted (12-JUN-2003) Takeshi Ito, Graduate School of
 Agriculture, Hokkaido University, Department of Applied Bioscience,
 Kita-9-jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan

(E-mail: hco-@abs.agr.hokudai.ac.jp, Tel: 81-11-706-2487 (ex. 2487))

FEATURES

Location/Qualifiers

1..4100

/organism="Bacillus thuringiensis serovar aizawai"

/mol_type="genomic DNA"

/strain="Bun1-14"

/serovar="aizawai"

/db_xref="taxon:1433"

267..273

/note="putative"

279..2279

/gene="cry40-like"

279..2279

/gene="cry40-like"

279..2279

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

/product="putative mosquitocidal toxin"

/protein_id="BAC77648.1"

/db_xref="gi:31745044"

/transl_table=1

301 TCTATATGATGATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGACGCTGTTAAGTAC 360

567 TCTATATGATGATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGACGCTGTTAAGTAC 626

361 GGGTTTCAGATTTTGGAGGTGAAATGACGCTTATCAAGATTATTTATCTTCAATTATCTT 420

627 GCGTATGAGAAATTTAATGATGATGAAATTTATCAATTTATCTTCAATTATCTT 686

421 GAGATGAGCTTACAG-----ATTAATCAAAATCTTAATAAACTTGTGACGTAGTAAA 474

687 AAGAAAGTGTATGACGAGGAAACCACTACGTGCACTACTTACGATGTAATCA 746

475 CAGTTCCAGCAGGAGAGAGATTGACTAACTTTAGCAGGCTATTATCAAGACAG 534

747 CATTTCGAATTTTACAGAAAGGAGATTCAATGACCTTCAAAAGGCTATTATCAAGACAG 806

535 AAGCTGAATTTATTTATTTGCTTACGATGATGACGCTGCAATTTGCAATTTTACTA 594

807 AAGGCTGAATTTATTTATTTGCTTACGATGATGACGCTGCAATTTGCAATTTTACTA 866

595 TTAAGGAGCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 654

867 TTAAGGAGCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 926

655 GGGTCAGGAGAA-----CTGATTTGTAACGAGGCTTTAAAGGCAAAATTA 702

927 GAATCGAATTTGATGACCTTTGTTGATTTAGAGGCAATTTCAAAAGCAATTAATCA 986

703 GAGTATCTAATTTATTTGATGAGGCTGATTAACAGGCTTTAGTCAATTAACAGGCG 762

987 GAGCATTTATATCTATTTATTAATCTGATCAGGCGGTTTAATCAGATTAAGAGATCG 1046

763 GGTACAGGCTGAGGCTTGTGGAATTTAATTAATTTGTGAGAAATGAGCTTGGCG 822

1047 GGTACAGGCTGAGGCTTGTGGAATTTAATTAATTTGTGAGAAATGAGCTTGGCG 1106

823 GATTTGATATTTATTTGCTATTTTCACTTATGATTTGAAATTTATCCATTAGCAACA 882

1107 GATTTGATATTTATTTGCTATTTTCACTTATGATTTGAAATTTATCCATTAGCAACA 1166

883 AGCTGATGATTTAATCTAGGAAATTTATCAAGATTCAGTGGATTTTCAAGGCGCAATTA 942

1167 CATATGAGTATTTAATCTAGGAAATTTATCAAGATTCAGTGGATTTTCAAGGCGCAATTA 1220

943 GGTGGGAGGTTTTTACCTTTAATTCGTTGAAGCAATGGAACAGCGGAGCTGGT 1002

1221 GAAACAAATCTTACCAATGTTTTAATGCTTGAAGCAATGGAACAGCGGAGCTGGT 1280

1003 TTAGTTACTTGGCTTCAAGCTATAGATATATATGATCTTATTAATCT----- 1052

1281 TTAGTTACTTGGCTTCAAGCTATAGATATATATGATCTTATTAATCT----- 1340

1053 -----TCAGCTTGGCTTATCTTATGCTGGGGGGAATCTGCTATTATGAAGCTTACA 1107

1341 TGGTCTCCTGCTATTTCTTAAAGGCTGGGCAAGCTGCTGCTATTATGAATTTATACA 1400

1108 AAGGTTACGCTGCTTCAAGGATGCTGGAATGCTGAAGTATGATATCAACGTAATTT 1167

1401 GGAAGTTCAATCTTTCGACGATATCTGGAATGCTGAAGTATGATATCAACGTAATTT 1460

1168 ATTATTTGCAATCCGATATATTTAAATTTATTTATCTGATATGATGCAAA--- 1224

1461 GATTTATCAATGATGATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1520

1225 ----CGTTTGTGGGATTTCAATCCACGCAATCTTTTCAAGTGCAGAAATTTTTCG 1281

1521 GCGGCTGCTGGTAACTTGAACCCAGGATTCGTTTGGGTGATGAAATTTATGATCG 1580

1282 ACAACATAATATCTTCTGATGAGGTAAAGTTCTGGG---TACTCAGACGAACTT 1338

1581 ACAGGAGATATCTTCTGATGAGGTAAAGTTCTGGG---TACTCAGACGAACTT 1640

ORIGIN

Query Match 39.8%; Score 803.6; DB 1; Length 4100;
Best Local Similarity 67.1%; Pred. No. 6.4e-145;
Matches 1348; Conservative 0; Mismatches 569; Indels 93; Gaps 11;

DBHSGCTCNGHNSGCTCNGYNR"

CDS

2348..3949

/note="ORF2"

/codon_start=1

/transl_table=1

/product="hypothetical protein"

/protein_id="BAC77649.1"

/db_xref="gi:31745045"

/transl_table=1

/product="hypothetical protein"

/protein_id="BAC77649.1"

/db_xref="gi:31745045"

/transl_table=1

/product="hypothetical protein"

/protein_id="BAC77649.1"

/db_xref="gi:31745045"

/transl_table=1

/product="hypothetical protein"

/protein_id="BAC77649.1"

/db_xref="gi:31745045"

/transl_table=1

/product="hypothetical protein"

/protein_id="BAC77649.1"

/db_xref="gi:31745045"

/transl_table=1

Db 1068 GATTGGAGAAATATCATTCAGACACAGTAGTAGTGAAGTCTAGGAAATTTATACAGAT 1127
Qy 916 CCAAGTGGATATTCAGGGGAAATTTATGTTGGAAACGTTTT-----TTAGCTTTAAT 969
Db 1128 GCAAGTGGATATTCATCGGAACTTATATGTTGGATAGCGAATTCCTTAATCTTTTAAAT 1187
Qy 970 TCGGTGGAAGCAATAGGACACGGGGACCTGTTTACTTACTTGGCTTCAAGCTATAGAT 1029
Db 1188 GGGTTTAGGCTATATGACACGGGGACCTGTTTACTTACTTGGCTTCAAGAAATAGGT 1247
Qy 1030 ATATATAGTCAATCTATATTAATCTTCAGCTTGTTAGTGGCTGGGGGAACTCGT 1089
Db 1248 ATATATATAGTATATGTT-----TCGAGATATTTTCCCGCTGGAGAGAACTCGT 1298
Qy 1090 CATTATGAAACCTTCAAAAGGGTATACGGCTTTTCAACGATATGCTGGAACCTAGAGT 1149
Db 1299 CATTATGAAACCTCAACAAAGGGTATACGGCTTTTCAACGATATGCTGGAACCTAGAGT 1358
Qy 1150 AATATATCAGCTATATATTTTGGCAATACCGATATATTTAAATTTATTTCAATTAAGCT 1209
Db 1359 AATGATATCAGTATATATTTTGGCAATACCGATATATTTAAATTTATTTCAATTAAGCT 1418
Qy 1210 AGATATGCAATGCAACCGTTGTTGGTATTCATCCACGGCATCTTGTTCACGTCGA 1269
Db 1419 A--TCATGAACCTAGTAGAGAGAGACTACCGCTAGACCAAGATATGCTGTTTCAAGGCA 1475
Qy 1270 GAATTTTTTCCGACAAACCTAAATACCTTCTGATAGAGTAAACAGTTCTGG--TAC 1326
Db 1476 GATTTTTCGTAGGGTAGGGGACCTGATTTAAATTTATATATGCAAGTATTAATAGGCTAAGC 1535
Qy 1327 TCACAGCAATATGTAATCTGTGTATACAGGATATTAATTAAGATCTACCACTAGTCGTACA 1386
Db 1536 AGATATGCAATTTAATCTAGCTTCCCACTTGT-----ATTGCACTTAAATGGTGTAGA 1589
Qy 1387 AATTAATCTCATAGATTTCAAAATGCGGCAATGTTTCAAAATGAAACCTCAGAGTTTAC 1446
Db 1590 GGAACCTCTCATAGATTTATCAAAATGCGGCAATGTTGTATATAGGAACTCAGAGTTTAC 1649
Qy 1447 GTATTTGGTGGACACATCAAGTATGAAAAAAGATATGAAATTTTCCAGATTAAT 1506
Db 1650 GTATATGTTGGACACATCAAGTATTAACGTAAGATTAATTAATGAAAGCAATCAAAAT 1709
Qy 1507 ACCGAAATTCCTGCAATTAAGCTTTGACCTTACCAAGGATACAGATATGACAGAGT 1566
Db 1710 ACACAATATCCGGCGGTGAAGAGTTTATTAACCTTCAAAATTAATCTTGTAAATGCTTATACC 1769
Qy 1567 TACGTACAGCTGGGCT 1584
Db 1770 TATGTATTAAGGCACT 1787

RESULT 8
CQ868314
LOCUS CQ868314 2073 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 15 from Patent WO2004074462.
ACCESSION CQ868314
VERSION CQ868314.1 GI:51998360
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 15 02-SEP-2004;
Athenix Corporation (US)
FEATURES
source location/Qualifiers
1..2073
/organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1428"

CDS 1..2073
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAH33952.1"
/db_xref="GI:51998361"
/translation="MSPYONKREYELILSSSNNTTPNRYPPANNRDMSTMSWDCOG
ISWDIMSEVETITISGINLIEFVIEPSLIGNTLLSTIGLIPNRQVSLSTCDL
LSITIREVADSVSDIADFDGKLNREYFVLSYIGAWLKDQKPLQKTNISDTGLVY
YKLSERDFNEILGSLSRNNAQVLLPFAQANVOLLLEDAVQAQWPLFSAE
NVRSELISNSGCDFTGDYERLKCKTAEYNYCDYQVGNQIKQGTGADTWSK
NKRREMTLAVDILAIPEYDFEKPLPTHELREIYTDAGVSSGTYSLRWMPN
TFNGEANGTGRGLVWMLSKIYNEVYSRFAQWGRHVEDYTKNGIQRWMSGT
TSDNIDIDFOADYKLTSLAIDMLVGETTARPERYSKDPFRVGGPDLDYDCN
GISRMTISSTFPLVHNSGRCPSRLSNAACTVYGNRVNYGTHSLKENTIEA
NQITQIPAVKSYIQNVLANATYVYIKGHTGDLIRPLRKSERYNAVYAGGILII
NKRAGOSYRIERFYADKAAPSVYVLPGGGNSRFPVLSKYSYGNDLKYSDPKF
AEIIPPLPSNVIQNDVEMQANSFQSDNVVLDKIEFLPSNTTILEYGERDLERTKN
AVNDLFTN"

ORIGIN
Query Match 36.6%; Score 739.8; DB 6; Length 2073;
Best Local Similarity 69.7%; Pred. No. 1.6e-132;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;
Qy 10 ATGAATCTTATCAAAATCAAAATGAATATGAAATTCGAGTGTCCCGGAATACACACA 69
Db 1 ATGAGTCATATCAAAATCAAAATGAATATGAAATTCGATCCATCGAATATACACA 60
Qy 70 AATATGTCAACAGATATCTTTTGGCAAGATCCAAATATATTTCTATTAACCTGAC 129
Db 61 AATAGCCCAACAGATATCTTTTGGCAATATTCGGAGATATCTATATATCTTGGAAT 120
Qy 130 GCTTGTACGGAAAGCCATGCAAGATACGTGGGAATCAGTCTCGAATATAGTAAT 189
Db 121 GATTTGCAAGGATCTCATGGGATGAATTTGGGAATCAGTCGAAACGATTAACAATAT 180
Qy 190 GGGACATACCTTATCAATCTTGTGAGAACCCGGATAGGGGAATTCCTGTAATATT 249
Db 181 GGGATTAATCTTATGAGATTTGAGTAGAACCTAGTTGGGGGAATTAATACATATTA 240
Qy 250 TCATATATTAACAACTCATCTTCCTGTCATCTGTGGACACATTTCTATATGT 309
Db 241 TCATATATGAAAACTATTCGACTATTCGTCAAACTGTGTGACACATTTCTATATGT 300
Qy 310 GATTTATGATATTAATTTGTAAGAGTAGACGAGCGGTGTAAGTACGCGGTTGCA 369
Db 301 GATTTATTAATTAATTTGTAAGAGTAGCGGATAGTGTAAAGTATGATGCAATTGCA 360
Qy 370 GATTTGAGGAGTGAATGATCTGCTTACAAATTAATTAATCTTATATCTGAGATTTGG 429
Db 361 GATTTGAGCGTAAATTTGAAATTAATGAGATTAATCTTATCTTATCTGGGCTTGG 420
Qy 430 CTTCAG-----ATAATCAATCTTAATAAACTTGCTGACGATGTTAA 474
Db 421 CTTAAGAGAGTAAACCACTTCAAAAAGCAAAATTAATTCGATATCGACAATTAAGTTAT 480
Qy 475 CAGTTCGAAGACGGGAGAGATTTCACTTAACTTTTACAGGGTCATTAATCAAGACG 534
Db 481 TATTTTAACTTTACAGAAAGAGATTTCAATGAAATCTGAGAGGGTCATTTGCAAGAAAC 540
Qy 535 AAAAGTGAATTAATTAATTTGCTAGTATGTCGAAGCTGCAAAATGCAATTAATTAATCA 594
Db 541 AATGCTCAAGTATGTTATTAATCTTATTTGCAAGAGTGAAGTATGAGTTATTAATCA 600
Qy 595 TTAAGGAGCGAGTAAATATAAAAAAGATGGGACCTAGTGTGCCACGGTTGTATCA 654
Db 601 TTAAGGAGTCACTTAATTAATTAAGCAATGTTCCCATTTTGAAGTCAAGAAATGTA 660
Qy 655 GGGTCAGGAGAA-----CTGATTTGAACGACGG 684
Db 661 AGATCGGAATTAATATCACTTAACAGTGTGTTGATTTACCGGTGATTAATGAGGCA 720

QY 685 TTAAGCGAAATTAAGAGTATCTAATTAATGTTGAGGCTGTATTAACAAGGTTTA 744
 DB 721 TTTAAATGCAAAACGGAGAGTATACCAATTAATGTTTAATGTTATCAGTAAGTTTA 780
 QY 745 GATCAGATTAAGACAGCGGGGTACAAGTGTCAAGTTTGGTCAAAATTAATTAATTCGT 804
 DB 781 AATATGATTAATAACAGGGGGGACAGGTGTCTCACTGTGTCAAAATTAATTAATTCGT 840
 QY 805 AGAGAAATGACGTTGGCGGTATGGAATTAATGCTAATTAATTCAGTATGATTTTGA 864
 DB 841 AGAGAAATGACGTTGGCGGTATGGAATTAATGCTAATTAATTCAGTATGATTTTGA 900
 QY 865 AAAATATCATTAGAACAGGTATGATTAATGGAATTAATTAATTAATTAATTAATTCGA 924
 DB 901 AAAATATCATTAGAACAGGTATGATTAATGGAATTAATTAATTAATTAATTAATTCGA 960
 QY 925 TATTCAGGGGAAATTAATGTTGGAACGGTTT-----TTAGCTTAATTCGGTGA 978
 DB 961 TATTCATCGGGAATTAATGTTGTTACGGAATTCGGCTAATTAATTCGGTGA 1020
 QY 979 GCAATATGAAACAGGGGACCTGTTTATGTTAATTCGCTCAAGCTATGATTAATTAAT 1038
 DB 1021 GCTAATGGAACAGGGGACCTGTTTATGTTAATTCGCTCAAGCTATGATTAATTAAT 1080
 QY 1039 CATTCATTAATCTTCAAGCTTGTATCTTAATGCTGTGGGGGGAATTCCTATTATGA 1098
 DB 1081 GAGTATGTT-----TCAGATTAATTTGCTCGGTGAGGAACTCGTATTATGA 1131
 QY 1099 GACTTCAAAAGGGAACGGGCTTCAAGCTATGCTGGAATTAAGGAATTAATTAATTAAT 1158
 DB 1132 GACTTCAAAAGGGAACGGGCTTCAAGCTATGCTGGAATTAAGGAATTAATTAATTAAT 1191
 QY 1159 CGTAATTAATTTTGGCAATACCGATTAATTAATTAATTAATTAATTAATTAATTAATGA 1218
 DB 1192 CGTAATTAATTTTGGCAATACCGATTAATTAATTAATTAATTAATTAATTAATTAATGA 1248
 QY 1219 ATGCAACCGTTTGGGTATTAATCCACCGCATCTGTTTCACTGCAAGATTTT 1278
 DB 1249 AACTTATGAGAGAGTACCGCTAGACACAGATGATGTTTCAAGGAGATTTT 1308
 QY 1279 CGCAACAATTAATCTTCTGTATGAGTAAACAGTTCTGGG---TACTCACAACA 1335
 DB 1309 AGGTATGAGAGAGTACCGCTAGACACAGATGATGTTTCAAGGAGATTTT 1368
 QY 1336 ATGGAATCTGTATGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1395
 DB 1369 ATGGAATCTGTATGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1422
 QY 1396 CATGATTAATTAATGAGGAGTGTCTCAAAATGAACCTTCAGAGTTAACTGATTTTGT 1455
 DB 1423 CATGATTAATTAATGAGGAGTGTCTCAAAATGAACCTTCAGAGTTAACTGATTTTGT 1482
 QY 1456 TGACACATTAATGAGGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1515
 DB 1483 TGACACATTAATGAGGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1542
 QY 1516 CTTGCACTAAAGCTTTGGCTTACAGAGTATGAGGAGTATGAGGAGTATGAGGAGTATGAGGAG 1575
 DB 1543 CCGGCGGTGAAGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1602
 QY 1576 GCTGGGCTT 1584
 DB 1603 AAAGGCACT 1611

RESULT 9

AB161456
 LOCUS AB161456 3931 bp DNA linear BCT 03-FEB-2004
 DEFINITION Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2
 complete cds.
 accession AB161456
 version AB161456.1 GI:41688282

KEYWORDS

Bacillus thuringiensis serovar entomocidus

Bacillus thuringiensis serovar entomocidus

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

REFERENCE

1 Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Amano, S.
 Cloning and Expression of Novel Crystal Protein Genes from Bacillus
 thuringiensis subsp. entomocidus INA288

2 (bases 1 to 3931)

AUTHORS

Tomonori, I., Kumiko, Y., Takeshi, I., Ken, S., Shin-ichiro, A. and
 Hisanori, B.

Direct Submission
 Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of
 Agriculture, Hokkaido University, Department of Applied Bioscience,
 Kita-9jo, Nishi-9choe, Kita-Ku, Sapporo, Hokkaido 0608589, Japan
 (E-mail: ikeyatn@agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
 Fax:81-011-706-2487)

FEATURES

source

1..3931
 /organism="Bacillus thuringiensis serovar entomocidus"
 /mol_type="genomic DNA"

/strain="INA288"
 /seovar="entomocidus"

/db_xref="taxon:1436"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

/gene="cry4Ba like"
 1..2061

ORIGIN

Query Match 10.6%; Score 214; DB 1; Length 3931;
 Best Local Similarity 69.0%; Pred. No. 3,6e-31;
 Matches 330; Conservative 0; Mismatches 130; Indels 18; Gaps 2;
 QY 1438 AGAGTAAAGTATGTTGTTGAGACATTAACAGTATTAATTAATTAATTAATTAATTAATTAAT 1497

Db 1594 ACACCTCAGATGTGCTTGAGACACATGTAAGCGGATCCGTATATAAGATTCA CCA 1653
Qy 1498 GATTAATTAAGCAATTCCTGAGTAAGCTTTTGCCCTACCAGCAGGTACAGATAT 1557
Db 1654 GATTAATTAAGCAATTCCTGAGTAAGCGGATCCGTATATAAGATTCA CCA 1704
Qy 1558 GCAGAGGTTACCTCAACAGCTGGCCCTGTTATACAGAGAGATAGTAAGTACCT 1617
Db 1705 GGGGAGGTGTAACCTGCTCTGACCTGTTTACAGAGAGCATTAGTAAGTACCT 1764
Qy 1618 TATCAAGCAAGTTAAATAATGCTTATCTTGACCCACGAATAATAATACCGTGT 1677
Db 1765 TATAATGACGTTGAAAAATACGTTAAATCCATACAGAGTAAAAATACCGTGT 1824
Qy 1678 AGAGCTGCTACAGCGAGTGAGAGACCTGCTCCGTTCCGATAGAAAGATGTCGCAAGT 1737
Db 1825 AGAGTGTGCTACAGATAGAGAGCTGCTACATACAGACAGAAAAATGTCGCGTAT 1884
Qy 1738 TCTGTTCAATGCTAATTTTCTGCTCAGCTACAGTGGCTATAGTTCAATTTGAT--- 1794
Db 1885 GGTAGGTATTTCTAATTTTGGGTATGATATACGGGTGATTCGATTAATTTAATAT 1944
Qy 1795 -----TATGTGACACCTTATGTAATCAATTAATCAATCAGGTGTTGAATATTA 1848
Db 1945 TTTAAATATTAGAACTTATCTGATCAATTTAAATATCTGCTGTTGAATAATTA 2004
Qy 1849 CAATATCTATCTGTTACACCTATTTGTTGACAAAGTGAATTTATCCCAATTGACA 1906
Db 2005 CAATATCTATCTGTTGCACTTATCTGTTGACAACTGTTAATTTATCAATTTAA 2062

RESULT 10
BTU88189
LOCUS 2028 bp DNA linear BCT 01-OCT-1998
DEFINITION Bacillus thuringiensis jegathesean insecticidal protein Jegt74 gene,
complete cds.
ACCESSION U88189
VERSION U88189.1 GI:3668334
KEYWORDS
SOURCE Bacillus thuringiensis serovar jegathesean
ORGANISM Bacillus thuringiensis serovar jegathesean
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Isolation and characterization of insecticidal genes from Bacillus
thuringiensis subsp. jegathesean
Unpublished
2 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Direct Submission
Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
Location/Qualifiers
FEATURES
source
1. .2028
/organism="Bacillus thuringiensis serovar jegathesean"
/mol_type="genomic DNA"
/sub_species="jegathesean"
/db_xref="taxon:56955"
1. .2028
/codon_start=1
/trna_table=1
/product="insecticidal protein Jegt74"
/protein_id="AAC61892.1"
/db_xref="GI:3668335"

CDS
1
/trna_table="ANPYQNKSECEILNPLNNINPNRYFPANDPNAVMKNGNYKDM
LNECDGTPSIFGLTGLVLAIVISTINLATPSIGAFALVSGYWPETKSPIS
VAVNRLIRBALDONAIRATGKNGIMOTVYVTKNLODWDPTEIPANPODSOLR
EABRSLETERPFRKALAGEFPAASQIVLLEIYAKANIHILLIKDMQRTDGL
IRRVGPVTTTASADPESEFLNRIKRTDCLISYVDGLAKISRSQSDETWNEFKP
RREMTLVLDLVALYPTNHLKLYPIQTELSRVYVTPDGCNGNSDIFSNLNDY
LENLRTLRPREPYNLSVOLFASTVSNNGEVLRLNLANIMEGKMTGSRSDGVT
GTFPTMDMSYGVGPRKHYAETISRSQALPLGNSIHVIGIDSPRALGPGGQDHT

Query Match 9.8%; Score 197.2; DB 1; Length 2028;
Best Local Similarity 54.6%; Pred. No. 7,4e-28;
Matches 524; Conservative 0; Mismatches 398; Indels 38; Gaps 5;
ORIGIN
FSLPGDMVDCQKVOINLEEDYRNSDHWISDMWTINOSVOLASNPOTFAPSAISLGM
HSSAGNNVYVYDKITQIPATKXRYRHPMKRGPEFTGSDLADLSSNDDICQDLSRD
YDDRITREVPFRIRLRCSISGVSTISVNNKSSSPQVYVASTASLSDTLKTESFOYVS
IPGNYPDSAPRIRILRPPGRLLVDRIEIIIVNFPFLESQENKSVDSLFIN
Qy 10 ATGAATTCCTTATCAAAATACAAATGAATATGAATTCGATGTTTCCCGAATTAACA 69
Db 1 ATGAATTCATACAAATGAATGAATGAATTAATTAATTCATTAATTAATTAACA 60
Qy 70 AATATGCAACAGATATCCCTTTTCCAAAGATATCCAAAT-----ATATTCC 116
Db 61 AATATGCAACAGATATCCCTTTTCCAAAGATATCCAAATTCGTGATGAAAAATGGGAAT 120
Qy 117 TATTAACCTGACGCTGTGACAGGAGCCATGACAGATACGTTGGAAATCAGTCCGA 176
Db 121 TATTAAGATGGTTGAATGAATGATGATATTAATCTCTTATTTTGGAAACATTGGA 180
Qy 177 TATTAAGATATGAGACATATCAATTCCTTGAAGACCCGGTATAGTGAAT 236
Db 181 GTTCTAGCAAGATATGATATTTCTATTAATCTTGCTACAGAGTCTTCCATAGAGAC 240
Qy 237 TCTGTATATTTTCAATTAATTAACAATCTACCTGCTTGTGCAATCTGTGACG 296
Db 241 GCAATTTGCTTATGATGATGATTTGAGAGATTTGGCGGAGACAGAACCTCGTTCC- C 299
Qy 297 ACTTCTATATGATATTAATTAATTTGTTAAAGGATGAGAGAGCGGTATTAAG 356
Db 300 TTGTCTGTAGCGGATGTAATCTGTTAATTCGTAAAGCGCTTGACCAAAAGCTATTA 359
Qy 357 TGACGGGGTTCAGATTTTGAAGTGAATGACCTGCTTACAAATTAATTAATCTTCA 416
Db 360 CAGGCAACGGGAAATTTAATCGTTTAAATGACACATATTAACGGTATACCTTA 419
Qy 417 TCTTGAGATTTGCTTACAGATTAATCAATTCCTTAAATCTTGCTGA-----CGTNG 469
Db 420 TCTCCAAATTTGATGATGATCTGCAATTCCTGCGAATCCTCAGGATGATCGACCTAG 479
Qy 470 TTAACAGTTCCAAACAG-----GGAACAAATTCACATTAATCTTTGACAG 518
Db 480 AGAAGCAGTTAAGAAAGCTTTGAAGACATTAAGAGATTTTGAAGAGCATAGCAG 539
Qy 519 GTCAATTAACAGACAGAAAGCTGAATATTAATTAATTCCTGATATGCAAGCTGCAA 578
Db 540 TGAATTTGCAAGCGGATGATCAATAGTATTAATTAATTTATGCAAGCTGCAA 599
Qy 579 TGTGATTTATTAATTAAGGACGCAATTAATTAATTAATTAATTAATTAATTAATTA 638
Db 600 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 659
Qy 639 TCCACCGTTGATCCAGGCTCAGGAGAACTGA-----TTGTAACGAGCGGTTAAAGC 692
Db 660 ACTGTAGGTGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 719
Qy 693 GAAATTAAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 752
Db 720 GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 779
Qy 753 AAGACAGCGGCTACAGTGTGAAAGTTGCTGAAATTTAATTAATTTGATGAGAAAT 812
Db 780 AGTTCAACAGGTTCAAGTGTGAAAGTTGCTGAAATTTAATTAATTTGATGAGAGAT 839
Qy 813 GAGTTGGGATTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 872
Db 840 GACATTAACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 899
Qy 873 ATTAAGCAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 932
Db 900 AATACCAACAAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 959

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3471)
Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A.
Toxins active against pests
Patent: JP 2001507208-A 42 05-JUN-2001;
MYCOGEN CORP
PN JP 2001507208-A/42
PD 05-JUN-2001
PF 01-JUL-1997 JP 1998504483
PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI
BRIAN A STOCKHOF
PC C12N15/32, C12O1/68, C12N15/82, C07K14/325, A01N63/00, A01H5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
1.3471 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 172.4; DB 6; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3.9e-23;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGAAATCAGTCTCGGATATAGTACTTATGAGACATCTTATATACATCTTCTGTAGAAC 220
158 GCGATGACGAAAGAAAGAGCATATCTATGAGACACCAATGCTCTTATACAGCAC 217
221 CCGGATAGGTGGAATTCCTGTAATATTTT-----CAATAATAAACAATCATTCGGT 274
218 CTCTCTTACTGATTAATTTCAATAGTATAGCCTTATAGGTAAGTACTAGAGGTA 277
275 CTTCGTGATCTGTGCGACGACCTTCTATATGTAATTAGTATCTATATTCGTAAG 334
278 GTAGTGAACATCATATACATGATGATGCTATATGTCATATATCTATATTTGATTTAC 337
335 AGGTAGACGAGCGTGTATAGTGAACGGGTGCGAATTTGAGGGGAATGACGCTT 394
338 GGGTATAGTCAGATGTTTAAATGATGAGATTGCAATTTAAATGTTCTGCTCTTAT 397
395 ATCAAGATTATATCTTC-----ATTATCTTGAGGATTTGCTTACAGATA 439
398 ACAGAACTATTATTAAGAGCTCTGATAGTGAATAGATTCCTAATTCGCTTCTGCTG 457
440 AATCAATCTTAAAAAATCTGTCGACGTACTTAAACGTTCCAAAGCAGGAAAGAGATT 499
458 AAGAACTCCGCTACTCGTTTAAATGCGCAGCTCAGATTGATAGATTTTTAAACCGAG 517
500 TCACTAACTTTAGCAGGGTCAATTAATCAAGAGAAAGCGAAATTTATTTATTTGCTTA 559
518 GGTCTTTAAGATGGGCTCGTTAGACCTAGCAAAAATGCCAAATTTTATTTATTTACTT 577
560 CGATGTGCAAGCTGCAATGTCATTTATTTATTTAGGAGCGCATTTAAATATATATAA 619
578 CTTTGTGAGCGCTGCAATTTTCCATTTATTTACTAAGAGATGCTACTAGATAGGCA 637
620 AAGAAATGGGACATGATGTGTCACCGTTGATTCAGGGGTCAAGGAAACGATTTGTAAC 679
638 CTAAATGGGGGCTATTCMAATGCTACACCTTTATTA-----ATTATCAAT 682
680 AGCGTTTAAAGGAAATTAAGAGATTAATTTATTTAGGTTGATTAACAGG 739
683 CAAACTAGTAGAGCTTATTTGAATATATCTGATTTTTCGTAATGTAATATATGAG 742
740 GTTTAGATGATATAGACAGCGGGTACAGATGCTGAAGTTTGTGCGAAATTTATTAAT 799
743 GTTTCAACGAATAGACAGAGCGCTAGTGTCTACAGCTTGTGTAATTTCAATGAT 802
800 TTGTTAGAAATAGAGCTTGGCGGTATGATATTTATTTGCTATATTTCCAACTTATGAT 859

Db 803 ATGTAGAGAGAGACATGATGATGATATATATAGATCATCATTTTCAAGCTTGATA 862
860 TTGAAAAATATCCATTAGACAAAGTGTAGATTAACTAGGAAATTTATACAGATCCAG 919
863 TTACTATATATCCCAATAGAAACGATTTTCAGTTGATGAGGTCATTTATACAGATCCA 922
920 TGGGATATTCAGGGGGAATTTATGTTGGAA 951
923 TTGTTTGTATCATCGTAGAGCTTAGGGGA 954

RESULT 15
BD128371
LOCUS
Toxin active on Oestrinianubialis.
BD128371
ACCESSION
BD128371.1 GI:23223316
VERSION
JP 2002500166-A/42.
KEYWORDS
unidentified
unidentified
unidentified
unclassified.
SOURCE
ORGANISM
1 (bases 1 to 3471)
Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and
Cohn, J.M.
Toxin active on Oestrinianubialis
Patent: JP 2002500166-A 42 08-JAN-2002;
MYCOGEN CORP
OS Unidentified
PN JP 2002500166-A/42
PD 08-JAN-2002
PF 15-DEC-1998 JP 2000526647
PR 31-DEC-1997 US 09/002285
PI ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI
BRIAN A STOCKHOF, JUDY MULLER COHN
PC A01N63/02//C07K14/325, C12N15/09, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Toxin active on Oestrinianubialis
FH Key Location/Qualifiers
FT source 1.3471
/organism="unidentified".
Location/Qualifiers
1.3471
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 8.5%; Score 172.4; DB 6; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3.9e-23;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGAAATCAGTCTCGGATATAGTACTTATGAGACATCTTATATACATCTTCTGTAGAAC 220
158 GCGATGACGAAAGAAAGAGCATATCTATGAGACACCAATGCTCTTATACAGCAC 217
221 CCGGATAGGTGGAATTCCTGTAATATTTT-----CAATAATAAACAATCATTCGGT 274
218 CTCTCTTACTGATTAATTTCAATAGTATAGCCTTATAGGTAAGTACTAGAGGTA 277
275 CTTCGTGATCTGTGCGACGACCTTCTATATGTAATTAGTATCTATATTCGTAAG 334
278 GTAGTGAACATCATATACATGATGATGCTATATGTCATATATCTATATTTGATTTAC 337
335 AGGTAGACGAGCGGTATAGTGAACGGGTGCGAATTTGAGGGTGAATGACGCTT 394
338 GGGTATAGTCAGATGTTTAAATGATGAGATTGCAATTTTAAATGTTCTGCTCTTAT 397
395 ATCAAGATTATATCTTC-----ATTATCTTGAGGATTTGCTTACAGATA 439
398 ACAGAACTATTATTAAGAGCTCTGATAGCTGAGAAATAGATTCCTAATTCGCTTCTGCTG 457

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:54 ; Search time 5407.27 Seconds

(without alignments)
17469.639 Million cell updates/sec

Title: US-10-782-141-2

Sequence: 1 gttcaaaatcgaattctta.....atagttattatcaattaa 2019

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	65.2	3.2	1101	10	CNS0039G
C 2	56.2	2.8	1101	10	CNS0183P
C 3	53.6	2.7	1101	10	CNS000D1
C 4	53	2.6	1101	10	CNS0100X
C 5	51.8	2.6	1204	10	CNS01652
C 6	51.4	2.5	1235	10	CNS0161D
C 7	50.6	2.5	928	10	CNS0102F
C 8	49.6	2.5	1101	10	CNS000E1
C 9	48.4	2.4	938	10	CNS000C7
C 10	48.2	2.4	1101	10	CNS0106X
C 11	47.2	2.3	1101	10	CNS00100
C 12	46.6	2.3	867	11	CNS075B6
C 13	46.4	2.3	572	3	BP256971
C 14	46	2.3	355	1	AA448366
C 15	46	2.3	511	6	CB158772
C 16	46	2.3	817	5	BU773209
C 17	46	2.3	1414	4	BC025177
C 18	46	2.3	7050	10	AY420513
C 19	45.8	2.3	764	9	B2025901
C 20	45.4	2.2	858	8	DR732187
C 21	45.4	2.2	1101	10	CNS017KX
C 22	45.2	2.2	350	10	N97363

23	45.2	2.2	583	9	BH725336	BH725336
24	45.2	2.2	1073	1	AJ928975	AJ928975
C 25	45	2.2	572	11	CR332988	CR332988
C 26	44.6	2.2	1092	10	CNS020K7	AL175696 Tetradon
C 27	44.6	2.2	1192	11	CNS03Y36	AL265803 Tetradon
C 28	44.4	2.2	550	5	BU778710	BU778710 SJREG804
C 29	44.4	2.2	559	5	BU777332	BU777332 SUREDA09
C 30	44.4	2.2	679	4	AY809710	AY809710 SCHISTOSO
C 31	44.4	2.2	681	7	CV697396	CV697396 SUS_031_5
C 32	44.4	2.2	834	4	AY811172	AY811172 SCHISTOSO
C 33	44.4	2.2	875	4	AY914981	AY914981 SCHISTOSO
C 34	44.4	2.2	1001	10	CNS0155H	AL105023 Drosophila
C 35	44.2	2.2	639	9	BZ836800	BZ836800 CH240_258
C 36	44.2	2.2	1031	10	CNS000C2	AL059199 Drosophila
C 37	44	2.2	435	3	BU015872	BU015872 BU015872
C 38	43.8	2.2	698	9	BH940326	BH940326 odg39c04.
C 39	43.8	2.2	918	10	CNS006MW	AL065768 Drosophila
C 40	43.6	2.2	387	5	BU495119	BU495119 PESTOab8
C 41	43.6	2.2	424	5	BQ586758	BQ586758 PESTOab2
C 42	43.6	2.2	583	5	BU498079	BU498079 PESTOab9
C 43	43.6	2.2	749	7	CK286885	CK286885 B57749607
C 44	43.6	2.2	790	10	CM496443	CM496443 FebD001f2
C 45	43.6	2.2	840	9	AZ685747	AZ685747 EMTLM94TR

ALIGNMENTS

RESULT 1
LOCUS CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921 GI:4941778
VERSION AL063921.1 GI:4941778
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
TITLE The determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
JOURNAL The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeegawa and Aaron Mammoeer in Pieter de Jong's laboratory in the department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelbac11.

Location/Qualifiers
1. .1101

```
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/at_c="5' 3' 2007
```

```
/db_xref="taxon:122/"
/clone="BACN37D10"
/clone_1:b-"DreCPAC"
```

```

/cione_id="p10bba"
/plasmid="pBelobac11"
/note="end : SP6"

```

/ scc - can . cc

ch	2.8%;	Score 56.2;	DB 10;	I
Similarity	20.8%;	Pred. No. 0.0093;		

123; Conservative 213; Mismatches 253; 1

21 GAGATTGGCTTACAGATAAATCAATCCTAAAAAATTGCTT

607 GAGAAATGGAGGAGGAAAAAATAAAAAAATAAAAAAAGGCGH

81 CAGCACGGGAAGAAGATTCACTAACTTTAGCAGGGTCT

```

667 GDATAATAAAAAAABDTKDRRDARGAARAAAAABAARRMA
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

```

```

361 GAAATATATATGCCACGATAGTCACGCTCCAAATGTC
      ||| | | | : | | : : : : |
327 AAAAAATCTCTTAAAAACGACGATGACATCCACAT

```

001 GAGGCACTTAATATTAAGAAATGCGGCACTTCTCTGCGA
 002 AAAAAATAGIINKIATUUUAAAGCGGCGI GAGGCAUUGGGA

001 GACCCGCGIATAAIAATAAAGAAATGGGACAAAGTGTGTCTC
87 BAAAAADAKRAAAAAAAAAAADACGKPKWKKGDF

GGGAGAACTGATTGTAAACGAGCGGTTAAAAGCGAAATATAAA

47 GTATAWTTWDAITWADTWKCAATDPAKRAAAGRRKRDARKTAH

21 GTAGGTGTATACCAAGGTTAGTCAGATAAGACAGGCC

```

: : | : | : : : : : | | | | :
307 RARAGARRARAARRAADDRDWDAAAAAAATTTW

```

781 TGGTCGAAATTTAATAAATTTCGTAGAGAAATGACGTTGGCC

```

367 AAWDDARARARRRRRRRRRRRARARADDTTDKRW

```

341 ATATTCCACTATGATTTGAAATATCCATTAGCAAC

027 WDKAKRDRWWAAKADGAWKWRDRARDWATAKDDDGWKDKK

900 -GGAATTATACAGATCCAGTGGATATTCAGGGGAATT

087 TKKDDDDWDKTWTRDWWWWWTRTKNDDWWDDGGRGRWTRR

59 TAGCTTATTGGTAGAAGCAATGGAACACGGGACCTC

047 KDTPTADKDKRTDTTKRDGDDWRKDKDKKRRDKKGGDDKTY

CNS000D1 1101 bp DNA 1

Drosophila melanogaster genome survey sequencer BACR01J16 of RPI-98 library from Drosophila

FLY), genomic survey sequence.
AL065414

AL065414.1 GI:4938827
GSS.

Drosophila melanogaster (fruit fly)
Drosophila melanogaster

Eukaryota; Metazoa; Hexapoda; Insecta; Ephemeroptera; Trichoptera; Lepidoptera; Neuroptera; Endopterygota; Diptera; Brachycera

REFERENCE
AUTHORS
TITLE
JOURNAL

Ephydroidea: Drosophilidae: Drosophila.
1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope (E-mail: seque@genoscope.cns.fr)

BP 191 91006 EVRY cedex - FRANCE

- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org/TheBDGP/Drosophila>

melanogaster BAC library was prepared by Kazutoyo Osogawa and

Aaron Mammeter in Pictet de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1. 1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_1lb="BACR01J16"

/note="end : TET3"

Query Match

Best Local Similarity 15.6%; Pred. No. 0.042;

Matches 71; Conservative 199; Mismatches 185; Indels 0; Gaps 0;

2.7%; Score 53.6; DB 10; Length 1101;

687 AAAAGCGAATAAAGATGATTAATTTGTTGAGGTTGTAACAAGGTTTGA 746

582 AAAAATAAATAAATAAAGATGATTAATTTGTTGAGGTTGTAACAAGGTTTGA 746

747 TCAAGTAAGCAGGCGGTCAAGTGTGAAGTTTGTCAAAATTTAATTAATTTCTAG 806

642 KKKRKKKKRAATDTATTAATTTGTTGAGGTTTGTCAAAATTTAATTAATTTCTAG 806

807 AGAATGACGTTGCGGTATTTGATTTGTTGAGGTTTGTCAAAATTTAATTTCTAG 866

702 AKBAKRWKDDDTKKTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 761

867 ATATTCATTGCAACAAGTGTGAAGTTTGAAGGAAATTTATACAGATCCAGTGGATA 926

762 RGRWGDKRRRTGARGDKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 821

927 TTCAGGGGGAATTAATTTGTTGAGGTTTGTCAAAATTTAATTTCTAG 966

822 WDTKTRGAKDADKKAAGKRRKMTTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 881

987 AACACGGGACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1046

882 WRRWRGADKKKKMDDDDTADKDWTKOTDTAGATGAGGTTGTTGTTGTTGTTGTTGTT 941

1047 TAAATTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1106

942 WKMGKRGDGGKRTAGAGDGGKKGKKGKKGKKGKKGKKGKKGKKGKKGKKGKKGK 1001

1107 AAAAGGTAACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1141

1002 RRAAGRGDRKGGDKKKRRARWRKGGKKGKKGKKGKKGKKGKKGKKGKKGKKGK 1036

RESULT 4

CNS0100X 1101 bp DNA linear GSS 26-JUL-1999

LOCUS Drosophila melanogaster genome survey sequence Sp6 end of BAC

DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL098379
AL098379.1 GI:5609990

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope (E-mail: seque@genoscope.cns.fr)

BP 191 91006 EVRY cedex - FRANCE

- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector

peloBAC11.

Location/Qualifiers

1. 1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_1lb="BACN03G04"

/clone_1lb="DrosBAC"

/plasmid="peloBAC11"

/note="end : Sp6"

Query Match

Best Local Similarity 16.2%; Pred. No. 0.059;

Matches 102; Conservative 259; Mismatches 267; Indels 1; Gaps 1;

2.6%; Score 53; DB 10; Length 1101;

578 ATGCGATTATTAATTAAGGAGCGAGTAAATTAATAAATAAGGAGCTAGTGT 637

451 DWMTDTKTTTWTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 510

638 GTCCACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 697

511 MANNAGMTWDXDKTKAKKRTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 570

698 TAAAGAGTAACTAATTAATTTGTTGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 757

571 ARADRAANAKDADKADTDATKTDGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 630

758 AGCGGGGTCAAGTGTGGAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 817

631 RRGWGWGKGGKKTATTK 690

818 TGGCGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 877

691 CGGDSKAGDRAWARRAKATRAAADAATAAATAATTAATTTGTTGTTGTTGTTGTTGTT 750

878 CAACAAGTGAAGTTAATTAAGGAAATTTATACAGATCCAGGATATTTGAGGGGAA 937

751 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 810

938 ATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 996

811 GKKAAGKDDHKAAMWADDTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 870

997 CTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1056

871 GRRKARGRRRGRRRDKKRRKRTKAGBDGAGTDAAGDKKADGGGKRRKWDK 930

1057 CTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1116

Db	931	TWAKTMTGDTDTTWWKGNRRGRBAGRGRRGRKGRKAGKAGKMMKMAADABWTMTW	990
Oy	1117	GGTGGCTTTCAACGTAGTGTCTGGAACCTACGAGTATATAATCCAGCTAATATTATTTGGC	1176
Db	991	DKMKMMKMTDTMGKGGGEMGGKRGAGADGAKRRNRKRDGMRYGNRAMKMWDDAATKAR	1050
Oy	1177	AATCCGCTATATTTAAATATTATTCATT	1205
Db	1051	WADDMDADYDDADADADYKKKATWMDSW	1079
RESULT 5			
CNS016E2/c			
LOCUS			
DEFINITION			
CNS016E2 1204 bp DNA linear GSS: 26-JUL-1999			
Drosophila melanogaster genome survey sequence T7 end of BAC			
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit			
fly), genomic survey sequence.			
AL106628			
AL106628.1 GI:5622852			
GSS.			
Drosophila melanogaster (fruit fly)			
Drosophila melanogaster			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
Ephydroidea; Drosophilidae; Drosophila.			
1 (bases 1 to 1204)			
Genoscope.			
Direct Submission			
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
Determination of this BAC-end sequence was carried out as part of a			
collaboration with the European Drosophila Genome Project (EDGP) -			
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC			
library (Dros BAC) was made by Alain Billaud at CEPH (Centre			
d'Etude du Polymorphisme Humain) with funding provided by a MRC			
project grant. The DNA was prepared from embryos by Alain Bucheton			
and Genevieve Payan. It has been constructed in the vector			
pBelobAC11.			
FEATURES			
source			
location/Qualifiers			
1..1204			
/organism="Drosophila melanogaster"			
/mol_type="genomic DNA"			
/db_xref="taxon:7227"			
/clone="BACN15A12"			
/clone_lib="DrosBAC"			
/plasmid="pBelobAC11"			
/note="end : 17"			
ORIGIN			
Query Match 2.6% Score 51.8; DB 10; Length 1204;			
Best Local Similarity 21.7% Pred. No. 0.12;			
Matches 98; Conservative 162; Mismatches 190; Indels 1; Gaps 1;			
Oy	450	TAAAAAATTGCTGCTGACGTATTTAAACAGTCCAGCACGCGGAGAAAGATTTCACATAACT	509
Db	1197	KAAWAAWAKAKAKWAKATAAKAAWAKAKWAKAAAAAAAAAAAAAAAAAKAAADAAAK	1138
Oy	510	TTTACGACGGTCATATCAAGACAGAAAGCTGAATATTATTATTCCTAGTATGTCGA	569
Db	1137	KKAAAAAAAAAKAADAAADAAAAAAAAAKAKAAAAAAAAADAAAKKAAAAAAAAAAAK	1078
Oy	570	AGCTGCAATGTGCATTTATTACTTTAAGGACGCACTTTAAATATAAA-AAGAAATGGG	628
Db	1077	WKATKKDDDDKDKAADAADAKKKKKAKADADADKDKKKAKADWDADADAAKKKKKAK	1018
Oy	629	GACTAGTGTGTCACCGTTGATCCAGGCTAGGAGAACTGATTTGAACAGCGGTTAA	688
Db	1017	KDKKKDDATADWAAKAKAKKKDKKAKKKDKKKAKKAKKKDKKKDKKKKKKKD	958
Oy	669	AAGCAAAATATAAGAGTATCTAATTATTTGTGTAGGGTGGATATAACAGGGTTAGTC	748
Db	957	KKAKKKKKAAADAAAAAAAAAKKKDKKDAKAAKAAKKKKDAKKKKAKKKDDAAWADA	898

Oy		749	AGATTAAACGCGGGGTACAGCTGTAAGTTCGTGAATTTAATAATTTGCTGAG	808
Db		897	DKAAAKKKAALKKKDDKKDAADKKAADAKKKDDRAAKAADKDAAKKMKKKKAGAAR	838
Oy		809	AAATGACGTTGGCGGTATTTGATATTAATTCATATTTCCACTATATGATTTTGAAAAAT	868
Db		837	AAAAGKKGGRKGGGAGGRRAAAAAGATWTWMTTKTKAGDAPATTTTKTTTWATKA	778
Oy		869	ATCATTAGCAACAAGTGTAGACTTAACCTAG	899
Db		777	GAWAKKTTRAAPAADARGKDAATTAAKAAPAG	747
<hr/>				
RESULT 6 CNS0161D/c				
LOCUS	CNS0161D	1225 bp	DNA	linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL106171			
VERSION	ALI06171.1	GI:5620504		
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.			
COMMENT				
<hr/>				
FEATURES	Location/Qualifiers			
source	1..1225			
	/organism="Drosophila melanogaster"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:7227"			
	/clone_1fb="BACN15C18"			
	/clone_1lb="DrosBAC"			
	/plasmid="PbeloBAC11"			
	/note="end : Sp6"			
<hr/>				
ORIGIN				
Query Match	2.5%;	Score 51.4;	DB 10;	Length 1225;
Best Local Similarity	25.3%;	Pred. No..0.15;		
Matches 193;	Conservative 158;	Mismatches 406;	Indels 5;	Gaps 1;
Oy		4	AAAAATTTGAAATTTCTATCAAAATATACAAATGAATATGAAATTCGCATGTTCCCGAAT	63
Db		1190	WWAAWMAAAAMWTTTATTAATAAAATATATATMATWTATTTATWWWAAAAAMTTTTTAATWT	1131
Oy		64	AACACAATATATGTCOAACAGATATCTTTTGCAAAGATGCCAATATATATTTCTATTAAAC	123
Db		1130	ATTWTATATATAAAAAATATTTATTTTWWMAAAWMAAAWMAAAWMAATTTWTWGAATATA	1071
Oy		124	CTGACCGCTTGTCCGGAAGCCATGCCAAGATATCGTGGGAATCATGCTCGGATATATGTA	183
Db		1070	AAATATATATATATATAAAATWAMAMWTTWMAAAATATATTTTTTTTTTTTAAAAAAAA	1011
Oy		184	ACTATTGGGACATATCCTTATCATCTTCTGTGACACC GGATATAGGTGGAATTCCTGTA	243
Db		1010	AAWMAAAWTAATATATATWATDAAMWMTWMAAAAAAAAAAATATATTTTATTTAMAWTTTTTTRAA	951

OY		244	ATA-----TTTCAGTAATAAACCAACCATCTCCGGCTTCCGGTGAACCTGCGAGCAGC	298
Db		950	AAMTMTTTTTTTTTTTWTTTAAAMAATWTATWTATTTRRRRAATMTTTTTTTT	891
OY		239	TTTCTATATGTGATTAGATCTATATAATCTGTAAGAAGGTAGACGACGCGTTAAGTG	358
Db		890	TTTTTTTTTATATTTTTTTTTTMYHTTYMTTHHHMMMMMMMMHMGGBGGGGGTT	831
OY		359	ACGGGGTTCAGATTTTGAAGGTGAATGACTGCTTATCAGATTATTATCTTCATATC	418
Db		830	TTTTKTKTTTCTKTCTTGTGATTTTAAAATTTTNRDPTWAAAAADDTWNKTKMTTH	771
OY		419	TGAGAGATTGGCTTACAGATAATCAAATCCTAATAAAAACTTGCACTAGTAAGTAAAGT	478
Db		770	TTKDCKMKMGMMNNMMVMVGGRTKTKTKTKDKGRRRGGMTDTPARAAAAAAAAGDA	711
OY		479	TCCAAGCAGGGAAGAATTTCACTAACTTTAGCAGGGTCATTATCAAGACGAAG	538
Db		710	RAAABABABRGAGGAGGAGGARGGARCAARDMAKANGMKRTATMRDRRAGG	651
OY		539	CTGAATAATTAATTATTTGCCCTACGATGTGCAGCTGCAAAATGTGCAATTATTACTATTA	598
Db		650	AGGTAATATTTTTTAAARMGKRRTTAAAMAAAAMAWTTATRTAAMAAAAATPAAAAA	591
OY		599	GCGAGCGACGTTAAATATATAAAAAAGATGGGACTGTGTCCACCCTGTTATCCAGGCT	658
Db		590	AAMWAAMAAAAATWAAAAAATGATGNMNGAGAMANNMNMGMTTGNNGNNGGCGG	531
OY		659	CAGGAGACTGATTTGTAAAGCGGCTTAAAGCGAAATAAAGATATCTAATTATT	718
Db		530	NGTGNMNNMMAMMCMNNANNNNNNNNTSKTKTNMNNMMAMMMVVNTNTMNNMMMNNA	471
OY		719	GTTAGGCGTGTATTAACAAGGCTTTAGATCAAGTAAAGCAGG	760
Db		470	AGVNMMNGNNGNAMAMNMNMNMANMNGGTTGNGANNMAMVGG	429
RESULT 7				
CNS0102F/c				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
JOURNAL				
COMMENT				
FEATURES				
Source				

ORIGIN	/note="end : 17"
Query Match	2.5%; Score 50.6; DB 10; Length 928;
Best Local Similarity	21.6%; Pred. No. 0.23;
Matches 121; Conservative 172; Mismatches 268; Indels 0; Gaps 0	
Qy	344 AGAGCGTGTAAAGGACGCGGGTTCGACATTTTGGAGGGGGAATGACGTCCTATCAAGTT 403
Db	922 AGACGMAWMMGWRMAATDTRWATMTYKAKWBGAGTTRATKARTARAGAGAKKMAWR 863
Qy	404 ATTATCTTCATATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAACTTGCTG 463
Db	862 ATTAAKMTBKGAKTTRADKDTGGTGTGWTGTRGRTGKKRRBAGDGTGDRPTR 803
Qy	464 ACGTAGTTAAACAGTTCACAGCAGGGAAGAAGATTTCACCTAACTTTTACAGGGTCAT 523
Db	802 RAGRAGRWAKAARAKTAAADWGMARWAMWAMADATGATAMWWATATTAATATT 743
Qy	524 TATCAAGACAGAAAGCTGAAATATTATTATTGCTAGCTATGTGCAAGCTCCAAATGTC 583
Db	742 AMARWRMDAAATGTGKMRGTGTAAKAGATKGMDTRADAKKAAAGTTATATKATATG 683
Qy	584 ATTATATTAATTAAGGAGCGCAGTTAAATTAATAAAGAAATGGGACATAGTGTCAC 643
Db	682 TAKRPAKAKAMATATYAKAGATATRAAAATGADWATATGWTAKATTTGATG 623
Qy	644 CGTTGTATCCAGGGTCCAGGAGAACTGTTTAAAGCGGTTAAAGCGAAATTAAG 703
Db	622 RKMTDKMRRTKDKDADTGRWMAATPMWGAADDMRDGRATGAGRRMDGMRPARADR 563
Qy	704 AGTATCTAATTAATTTGTGTAGGGGTGTATTAACAAGGTTTGAATCAGATTAAGAAGCGGG 763
Db	562 TRKGAADRRGAAAAAAGTGTGADADKRAARBKODGDKRKTGKRAATGWRGAGRA 503
Qy	764 GTACAAGTGTGGAAGTTGGTTCGAAATTAATAATTTCCGAGGAAATGACGTTGGCGG 823
Db	502 KDGRKRMGWRKKKAKADKTKTMDTDTDKAKAAATGAKODGAKRMVGDGRKKGGGGAG 443
Qy	824 TATGATATTAATGCTATATTTCCAACTTATTTGAAATTTATTCATTAGAACAA 883
Db	442 ATATRTGGMWDMWATTTGATWTTATGRTATTKMAAGATTTAKAAGRAARAAMGAAA 383
Qy	884 GTGTAGATTAACTAGGGAAA 904
Db	382 AAKGAGAAKAKRAAAAAAAA 362
RESULT 8	
CNS00ESI/LOCUS	1101 bp DNA linear GSS 04-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR23L15 of RPI1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL069797
VERSION	AL069797.1 GI:4949738
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS	1 (bases 1 to 1101)
TITLE	Genoscope.
COMMENT	Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 9106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila

KEYWORDS	AL098595.1	GI:5610206
SOURCE	GSS.	
ORGANISM	Drosophila melanogaster (fruit fly)	
REFERENCE	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridiida; Drosophilidae; Drosophila. 1 (bases 1 to 1101)	
AUTHORS	Genoscope.	
TITLE	Direct Submision	
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.	
FEATURES	Location/Qualifiers	
source	1..1101 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACN03K20" /clone_1fb="DrosBAC" /plasmid="pBelobAC11" /note="end : 77"	
ORIGIN		
Query Match	2.4%; Score 48.2; DB 10; Length 1101;	
Best Local Similarity	19.1%; Pred. No. 0.95;	
Matches 107; Conservative 227; Mismatches 220; Indels 7; Gaps 2;		
QY	361 GGGGTTCAGATTTGGAGCGTGAAATGACTGCTTATCAAGATTAATCTTCATTATCTT 420	
DB	547 GKGCTCGACAGRGRTGCVKKEKHTHHWTGKKHTCTCHKHTTWTMTTWAKKGTG 606	
QY	421 GAGATTCGCTTACGATTAATCAATCTCTAAATCTTGCGACGTGTAATCAACGTTC 480	
DB	607 TGTDDKATKATMATGATGTAATRTTAAATKTAATKTAATDGTATTAATATKATKKARXKD 666	
QY	481 CAAGCAGCGGAAGAATTTGACTTAACTTTAGCAGCGTCAATTAACAAGACAGAACT 540	
DB	667 TADKAMKMDKATKAKAKKAKAKAKAAKATATGADAKAKAKAKAKATKAKARAWTJA 726	
QY	541 GAAATATTATTATTGCTTACGTATGTGCAAGCTGCAAAATGTGCATTATTACTATTAAAG 600	
DB	727 TWTATTAADAAADK---GAKDKAKAKAKADADBDKRRWDAKDKKRAKAKAAKADADA 782	
QY	601 GAGCAGTTAATATTAATAAAGAAATGGGGAAGTACGTGTCCACCGTTGTATCCAGGCTCA 660	
DB	783 DAKAKADAAKADKADADADDERGGKKKRAADRRKKKKKRAWDKKKAK--KDKAAA 839	
QY	661 GGGAGAACTGATTGTAACGACGGTTTAAAGGAAATTAAGATTAATAATTATTTGT 720	
DB	840 KAKADAAADGAKARRRABDDKAKADAAKAKAKAKAKDDDKAAATKAKATKAKKDKAKA 899	
QY	721 GTAAGGTGTATTAACAAGGTTTAAATGATCAGATTAAAGCAGCGGCTACAAAGTCTGGAAGTT 780	
DB	900 KKKKKKKDKDAAKAKAKADKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDD 959	
QY	781 TGTGTGAATTTAATTAATTTTCGTAGAAATGACGTTGGCGGTATTGGATTTATTTGCT 840	
DB	960 KAKDKDKDKDADAAKAAKADADDAKAKAKAKAAADDDAAADKAAADAAKAKAKAKA 1019	
QY	841 ATATTTCCAACTTATGATTTGAAAAAATATCCATTAAGCAAGCTAGAGATTAATCTAG 900	
DB	1020 DDAKAKAKAKADADADAKAKAAKAKAKATADADAAKAKAKADKDDKDDKDDKDDKAKK 1079	
QY	901 GAAATTTATACAGATCCAGTGTG 921	

Db		1080 AKADAAKAKAKAKAKKD	1100	
	RESULT 11	CNS00LO/c		
	LOCUS	CNS00LO/c	1101 bp	DNA linear GSS 03-JUN-1999
	DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR3D23 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
	ACCESSION	AL068607		
	VERSION	AL068607.1	GI:4958689	GSS.
	SOURCE	Drosophila melanogaster (fruit fly)		
	ORGANISM	Drosophila melanogaster Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101) Genoscope. Direct Submission		
	REFERENCE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
	AUTHORS	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.		
	JOURNAL	Location/Qualifiers		
	FEATURES	Source		
		1..1101		
		/organism="Drosophila melanogaster"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:7227"		
		/clone="BACR3D23"		
		/clone_1fb="RPc1-98"		
		/note="end : TET3"		
	ORIGIN			
		Query Match	2.3%; Score 47.2;	DB 10; Length 1101;
		Best Local Similarity	20.2%; Pred. No. 1.7;	
		Matches	96; Conservative	156; Mismatches 221; Indels 0; Gaps 0;
Oy		666 AACTGATTTGAAGCAGCGGTAAAAAGAAAATAAAGAATTACTTAATTGGTAGG	725	
Db		897 WDMWDARKKQDKDTKKKKKGKAGRAAAABDPAAMTKTXXKAKTWKG	838	
Oy		726 GTGCTAATAACAAGGTTTGATCAGATAAACAGCCGGGTCAAGTCGAAGTTGGTC	785	
Db		837 KKKGGGGRKTGGTGGKGGGTGAAGTCKKKKGGKGGTGDKKRTWMTTYTGYGTGT	778	
Oy		786 GAATTTAAATAAATTTGTTGTAAGAATAAGCATGGGCGGTATTTATTTATTTATTT	845	
Db		777 AMKTGKKKKKKKKKKKKKRWYTGTRMPTKYTKGSKTGSGGGKKTXYTKGKTWWA	718	
Oy		846 TCACAATTATGATTTGAAAATAATTCATTACCAACAAGTGATGATTTAACTAGGAAT	905	
Db		717 AWRAKKTKTKTKTKTKTKTAKTADTKTKKKKKDDKGTGCKWKXGDKAAMWGTDTRTXDK	658	
Oy		906 TTATACAGATCCAGTGGATATTCAGGGGAAAATTATGTTGGAAAGCTTTTTTACCT	965	
Db		657 KCAPAAPNDITDGKTKAKADRADTKGKAATKAAKAAAGMDADADGDTKKAATGTGT	598	

Oy		966	TAAATCGGTAGACGAATAANGAACGGGAGACTGGTTTAGTCTTGTCGCTTAAGCAT	1025
Dd		537	KADDTGGKAGARGGKGKKRKDKGAAGDGCATGATGAKKGTGATKKGDDKKRDPDGG	538
Oy		1026	AGATTATATATAGTCATTCATTATTAATCTTCAGCTGGTATCTAGTGTGCTGGGGGGAAC	1085
Dd		537	ARTKRGKKKKKGTGKTGKTKKDKGTDKKGRITDKGATRGRTGBKAGDAKGDGAGDGTGTGTGKCAR	478
Oy		1086	TCGTCATTATGAGAAGCTTCACAAAGGCTPAACGGTCCCTTTCAACGTATGTGGA	1140
Dd		477	GKAAAGCAGVAGARFAGAGAGAGAKRGGTGTGTGKKAGCGMGCRKDAGWGKAAR	423
<hr/>				
RESULT 12				
CNS075Bg/c	LOCUS	CNS075BG	867 bp DNA linear GSS 07-JUL-2001	
DEFINITION	clone BA0AB034D05 of library BA0AB from strain CLIB 210 of			
ACCESSION	Kluyveromyces lactis, genomic survey sequence.			
VERSION	AL429890			
KEYWORDS	AL429890.1 GI:12213084			
SOURCE	GSS.			
ORGANISM	Kluyveromyces lactis			
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
AUTHORS	Saccharomycetales; Saccharomycetaceae; Kluyveromyces. 1 (bases 1 to 867) Soucier,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojotin-Pikuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,U., Dujon,B., Durans,P., Lapingle,A., Lorente,B., Maurer,Y.A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekari,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.			
TITLE	Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies			
JOURNAL	FEMS Lett. 487 (1), 3-12 (2000)			
PUBMED	11152876			
REFERENCE	2 (bases 1 to 867) Bojotin-Pikuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Ngyuyen,G., Lemaitre,M., Marmelise,R., Montrocher,R., Robert,C., Termler,M., Wincker,P. and Wesolowski-Louvel,M.			
AUTHORS	Genomic exploration of the hemiascomycetous yeasts : 1. Kluyveromyces lactis FEMS Lett. 487 (1), 66-70 (2000)			
TITLE	11152886			
JOURNAL	3 (bases 1 to 867)			
PUBMED	Genoscope.			
REFERENCE	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, Direct Submision			
AUTHORS	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : beqef@genoscope.cns.fr Web : www.genoscope.cns.fr)			
JOURNAL	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.			
COMMENT	Location/Qualifiers			
	1..867			
FEATURES	/organism="Kluyveromyces lactis"			
source	/mol_type="genomic DNA"			
	/strain="CLIB 210"			
	/variety="lactis"			
	/db_xref="taxon:28985"			
	/clone="BA0AB034D05"			
	/clone_1fb="BA0AB"			
ORIGIN				
Query Match	2.3%	Score 46.6;	DB 11;	Length 867,
Best Local Similarity	39.7%;	Pred No. 2.3;		

Matches	229;	Conservative	31;	Mismatches	316;	Indels	1;	Gaps	1;
Qy	411	TCATTATCTTGAGGATTGGCTTACAGATTAATCAATCTTAAAAAACTGTCAGTAGT	470						
Db	579	TAAATTATATATATATTAATAAGAAAAAKAAAKAAATAATATKAAAKATATAAAAA	520						
Qy	471	TAAACAGTTCACACACGGGAAGAGTTTCACTAACTTTTACGAGGTCAATTATCAAG	530						
Db	519	TAAATTAATTTATATAAAAATGATATTAATAATGATATTAATTAATTAATTAATTAAT	460						
Qy	531	ACAGAAAGCTGAATATTTATTTATGCTAGCATATGTCAGACGTGCAATGCAATTAAT	590						
Db	459	AAATATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	400						
Qy	591	ACTATTAAGGACGACAGTTAAATATATAAAAAGATGGGAGCTAGTGTCTCACCGTTGA	650						
Db	399	TTTCTTAAAT	341						
Qy	651	TCCAGGCTCAGGGAAGAACTGATTGTATACGACGGCTTAAAGCGAAATTAAGAATAC	710						
Db	340	TTAAAKAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	281						
Qy	711	TAATTTATGTTAGGGGTATATATCAAGGGTTTATGATCAGATTAAGACAGCGGGTACAG	770						
Db	280	AKAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	221						
Qy	771	TGCTGAAGTTTGGTCGAAATTTATATTAATTTTCGTAGAGAAATGACGTTGGCGTATTTGA	830						
Db	220	TATATATATTTTATTTATTAAGAAAAATTAATTTTAAATTAATTAATTAATTAATTAAT	161						
Qy	831	TATTATTGCTATATTTCCAACTTATGATTTTGAATAATTCATTAGCAACAGTGTAGA	890						
Db	160	TTATTTATTTTCTTAT	101						
Qy	891	GTTAATACAGGAATTTATATCAGATCCAGTGGCATATTCAGGGGAATTAATGTTGTGA	950						
Db	100	KTTAKATTAATTTTAT	41						
Qy	951	ACGGTTTTTTAGCTTTAATTCGTAGAGCAATATGA	987						
Db	40	AATTAATTTGATATGATTTTAAATTTAAATTAATTAATTAATTAATTAATTAATTAAT	4						

RESULT 13

BP256971

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

source

BP256971 572 bp mRNA linear EST 16-SEP-2004

BP256971 Sugano cDNA library, kidney epithelial cell Homo sapiens

CDNA clone HNC1957, mRNA sequence.

BP256971

BP256971.1 GI:52172201

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 572)

Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,

Mitsushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1..572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

ORIGIN
 /clone="HRC12957"
 /tissue_type="kidney"
 /cell_type="epithelial cell"
 /clone_lib="Sugano cDNA library, kidney epithelial cell"

Query Match 2.3%; Score 46.4; DB 3; Length 572;
 Best Local Similarity 49.6%; Pred. No. 2.3;
 Matches 119; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 386 TGACCTGTTTCAAGATTATTTATCTTATCTTGAAGATTGGCTTACAGATTAATCA 445
 Db 8 TTATGCTTTATGCGAATCTCAGATCTGTTGCTTTGGAGAACTGAGAACAAAGAA 67
 QY 446 ATCTTAAAACTTGTGACGTTAAGAGTTTCAAGACGGGAGAAAGATTTCCTA 505
 Db 68 TTATATAGTACTAGATGAAATAGTGAAGAGTGAAGCCAAAGCCAAATTTGAAC 127
 QY 506 AACTTTAGACAGGCTCTTTATCAAGACAGAAAGCTGAAATTTATTTGCTTACGATG 565
 Db 128 GCCAGCGCTGAGGATATGAACTGACACAGAAAGCTGAGCAAGTTTATGTTAAAGCTG 187
 QY 566 TGCAAGCTGCAAAATGTCATTTATTTACTATTAAAGGACGAGTTAATATTAAGAAAT 625
 Db 188 AACAGCTATGAGAGAGATTGACGATTGACAGAGACACTGATTAAGCCAAACAGCAAT 247

RESULT 14
 AA448366 355 bp mRNA linear EST 04-JUN-1997
 LOCUS z996c06.r1 Soares total_fetus_Nb2H8_9w Homo sapiens cDNA clone
 DEFINITION IMAGE:784810 5' similar to gb:X66397_cds1 TPR ONCOGENE (HUMAN);
 mRNA sequence.
 AA448366
 VERSION AA448366.1 GI:2162036
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 355)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellenberg, K., Stepcoe, M., Tan, F., Theising, B.,
 White, Y., Wyllie, T., Waterston, R. and Wilson, R.
 Washu-Merck EST Project 1997
 Unpublished (1997)
 TITLE JOURNAL
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.lml.gov) for further information.
 Seq primer: -28ml3 rev2 ET from AmerSham.
 Location/Qualifiers
 1..355
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5982428"
 /db_xref="taxon:9606"
 /clone="IMAGE:784810"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares total_fetus_Nb2H8_9w"
 /note="Vector: pRT7D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAGTGGAGGCGCGCTTATTTTTTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors

FEATURES

source

ORIGIN
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match 2.3%; Score 46; DB 1; Length 355;
 Best Local Similarity 49.6%; Pred. No. 2.6;
 Matches 118; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 388 ACTGCTTATCAATATTTATTTCTTATCTTGAAGATTGGCTTACAGATTAATCAAT 447
 Db 23 AATGCTTATGCGAATCTCAGATCTGTTGCTTTGGAGAACTGAGAACAAAGAAAT 82
 QY 448 CTTAAAACTTGTGACGTTAAGAGTTTCAAGACGGGAGAAAGATTTCCTA 507
 Db 83 AATTAAGTACTAGATGAAATAGTGAAGAGTGAAGCCAAAGCCAAATTTGAAC 142
 QY 508 CTTTATGACAGGCTCTTTATCAAGACAGAAAGCTGAAATTTATTTGCTTACGATG 567
 Db 143 CACCGTGAAGATATGAACTGACACAGAAAGCTGAGCAAGTTTATCTGTTAAGCTTGA 202
 QY 568 CAAGCTGCAAAATGTCATTTATTTACTATTAAAGGACGAGTTAATATTAAGAAAT 625
 Db 203 CAAGCTATGAGAGAGATTGACGATTGACAGAGACACTGATTAAGCCAAACAGCAAT 260

RESULT 15
 CB158772 511 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0218180 L18POOLn1 Homo sapiens cDNA clone L18POOLn1-14-D04
 DEFINITION 5', mRNA sequence.
 CB158772
 ACCESSION CB158772.1 GI:28143910
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 511)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 TITLE JOURNAL
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 14 row: D column: 04
 High quality sequence stop: 511.
 Location/Qualifiers
 1..511
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOLn1-14-D04"
 /cell_line="SNU-354+Cho-CK+Cho-CK+HLK-3"
 /lab_host="Top10F"
 /clone_lib="L18POOLn1"
 /note="Organ: Liver; Vector: pRT73-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 6(9): 791-806. RNA was prepared from harvested cell
 culture."

FEATURES

source

ORIGIN
 Query Match 2.3%; Score 46; DB 6; Length 511;

Best Local Similarity 49.6%; Pred. No. 2.8; Mismatches 120; Indels 0; Gaps 0;
 Matches 118; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
 QY 388 ACTGCTTATCAAGATTATATCTTCATTACTTGAAGATTGCTTACAGATAATCAAA 447
 186 AATGCTTATGTGAACTCAGATCAGTTGCTTTGGAGAACTAGAGAACAAAGATT 245
 QY 448 CCTAAAAAAGCTTCTGACGTAGTTAAACAGTTCCAAAGCAGGGAAGAGATTCACTAAA 507
 246 AATTAAGTACCTAGATGAAATAGTGAAGAAGTGAAAGCCAAAGCCTTAATTTGAAACGC 305
 QY 508 CTTTTCAGAGGTCATTATCAAGACAGAAAGCTGAATATTTATTGCTTACGTATGTG 567
 DB 306 CAGCGTGAAGAAATATGAACGTGCAAGAAAGCTGTAGCAAGTTATCTGTAAAGCTTGAA 365
 QY 568 CAACTGCAAAATGTGCAATTATTACTATTAAAGGACGCAAGTTAAATATATAAAAAAGAT 625
 DB 366 CAAGCTATGAAAGAGATTGACGATTGACAGAGAGACATGATTAAGCCAAACAGCAAT 423

Search completed: December 19, 2005, 12:54:29
 Job time : 5410.27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 02:23:18 ; Search time 810.703 Seconds
(without alignments)
16597.955 Million cell updates/sec

Title: US-10-782-141-2

Sequence: 1 gtcgaataatgcattctta.....atagttattcatcaattaa 2019

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: geneseq11980s:*
2: geneseq11990s:*
3: geneseq12000s:*
4: geneseq12001as:*
5: geneseq12001bs:*
6: geneseq12002as:*
7: geneseq12002bs:*
8: geneseq12003as:*
9: geneseq12003bs:*
10: geneseq12003cs:*
11: geneseq12003ds:*
12: geneseq12004as:*
13: geneseq12004bs:*
14: geneseq12005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	2019	13	Adt899414 AXMI-008
2	2019	100.0	2145	13	Adt899413 AXMI-008
3	2010	99.6	2010	13	Adt899416 AXMI-008
4	747.2	37.0	2082	13	Adt899401 AXMI-008
5	747.2	37.0	5980	13	Adt899400 AXMI-008
6	739.8	36.6	2073	13	Adt899403 AXMI-008
7	174	8.6	1983	3	Aaz93234 Sequence
8	174	8.6	3837	3	Aaz93235 Sequence
9	172.4	8.5	3471	2	Aax16515 DNA encod
10	172.4	8.5	3471	2	Aax16515 DNA encod
11	162.8	8.1	2407	4	Aas02478 B. thurin
12	133.6	6.6	4391	14	ABE61394 B. thurin
13	119.8	5.9	1959	4	AAS02466 B. thurin
14	118.4	5.9	1986	4	Adt899411 AXMI-009
15	118.4	5.9	2016	13	Adt899409 AXMI-009
16	118.4	5.9	2049	13	Adt899407 AXMI-009
17	118.2	5.9	3687	12	Adt89478 B. thurin
18	118.2	5.9	3932	2	AAG64112 CRYETS ge
19	118.2	5.9	3932	2	Aaz09160 B. thurin

20	118.2	5.9	3934	2	AAT95051 DNA encod
21	118.2	5.9	3934	2	Aat68434 CRYETS ge
22	118.2	5.9	3934	2	Aav83927 DNA encod
23	117.6	5.8	1806	13	Adt899392 AXMI-004
24	117.6	5.8	1890	13	Adt899390 AXMI-004
25	117.6	5.8	2190	13	Adt899389 AXMI-004
26	116.8	5.8	3684	2	AAT95222 Bacillus
27	116.8	5.8	3684	4	AAS02489 B. thurin
28	113.4	5.6	2019	8	ABV93759 Nucleotid
29	113.4	5.6	3687	4	AAS02482 B. thurin
30	112.4	5.6	4173	4	AAS02482 B. thurin
31	112.4	5.5	1897	3	AAT93905 B. thurin
32	111.8	5.5	1897	3	AAT93905 B. thurin
33	111.8	5.5	1897	3	AAT93905 B. thurin
34	111.8	5.5	1897	3	AAT93905 B. thurin
35	111.8	5.5	2019	8	ABV93756 Bacillus
36	111.8	5.5	2019	8	ABV93757 B. thurin
37	111.8	5.5	3471	2	AAT93757 B. thurin
38	111.8	5.5	3471	2	AAT93757 B. thurin
39	111.8	5.5	3471	4	AAS02477 B. thurin
40	111.8	5.5	3471	4	AAS02477 B. thurin
41	111.8	5.5	4344	2	AAS06782 Insectici
42	111.8	5.5	4344	2	AAS06782 Insectici
43	110.2	5.5	2019	8	ABV93758 B. thurin
44	107.8	5.3	2160	4	AAS04855 Bacillus
45	107.8	5.3	2965	2	AAG06636 Gene enco

ALIGNMENTS

RESULT 1	
ID	ADR899414 standard; cDNA; 2019 BP.
XX	ADR899414;
XX	18-NOV-2004 (first entry)
XX	AXMI-008 coding sequence.
DE	
XX	bs: gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW	expression cassette; transformation; transgenic; plant; bacteria;
KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KW	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..2019
FT	/*tag= a
FT	/product= "AXMI-008"
FT	/transl_except= pos:1..3, aa:Met
XX	
XX	WO2004074462-A2.
XX	
XX	02-SEP-2004.
PF	20-FEB-2004; 2004WO-US005829.
XX	
XX	20-FEB-2003; 2003US-0448632P.
XX	20-FEB-2003; 2003US-0448633P.
XX	20-FEB-2003; 2003US-0448797P.
XX	20-FEB-2003; 2003US-0448806P.
XX	20-FEB-2003; 2003US-0448810P.
XX	20-FEB-2003; 2003US-0448812P.
XX	20-FEB-2004; 2004US-00781979.
XX	20-FEB-2004; 2004US-00782020.
XX	20-FEB-2004; 2004US-00782096.
XX	20-FEB-2004; 2004US-00782141.
XX	20-FEB-2004; 2004US-00782570.
XX	20-FEB-2004; 2004US-00783417.

PA (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;

XX MPI, 2004-635574/61.

DR P-PSDB; ADR89415.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 26; 178bp; English.

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SQ Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;

Query Match 100.0%; Score 2019; DB 13; Length 2019;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAAATATGTAATCTTATCAAAATCAATGAATGAAATTCGATGTTCCCG 60
DB 1 GTGAAATATGTAATCTTATCAAAATCAATGAATGAAATTCGATGTTCCCG 60
QY 61 AATAACAATAATGTCAAACAGATATCCTTTGCAAGAGATCCAAATATATTCCTATT 120
DB 61 AATAACAATAATGTCAAACAGATATCCTTTGCAAGAGATCCAAATATATTCCTATT 120
QY 121 AACCTGACGCTTGTGAGGAGAGGCGATGCAAGATACGTGGAAATCGATGATATA 180
DB 121 AACCTGACGCTTGTGAGGAGAGGCGATGCAAGATACGTGGAAATCGATGATATA 180
QY 181 GTAACTATTTGGGACATACCTTATCAATTTCTGTAGAACCCGGTATAGGTGAATTCCT 240
DB 181 GTAACTATTTGGGACATACCTTATCAATTTCTGTAGAACCCGGTATAGGTGAATTCCT 240
QY 241 GTAAATTTTTCATTAATTAACAACATCTCGCTTCGTGTAATCTGTGGAGACATT 300
DB 241 GTAAATTTTTCATTAATTAACAACATCTCGCTTCGTGTAATCTGTGGAGACATT 300
QY 301 TCTATATGTAATTTAGTATCTAATATTCGTAAGAGGTAGACGAGCGGTAAAGTAGAC 360
DB 301 TCTATATGTAATTTAGTATCTAATATTCGTAAGAGGTAGACGAGCGGTAAAGTAGAC 360
QY 361 GGGGTTGCAAGATTTTGAAGGTGAATGATGCTTATCAAGATTATATCTTCATTTCTT 420
DB 361 GGGGTTGCAAGATTTTGAAGGTGAATGATGCTTATCAAGATTATATCTTCATTTCTT 420
QY 421 GAGGATTTGGCTTACAGATTAATCAATCTTAAACCTTGCATGATGTAACAGTTTC 480
DB 421 GAGGATTTGGCTTACAGATTAATCAATCTTAAACCTTGCATGATGTAACAGTTTC 480
QY 481 CAAGACGAGGAGAAAGATTCACTAACTTTAGCAGGAGCATTAACAAGAGAAAGCT 540
DB 481 CAAGACGAGGAGAAAGATTCACTAACTTTAGCAGGAGCATTAACAAGAGAAAGCT 540
QY 541 GAAATTTATTTATGCTTACGATATGTCAGAGCTGCAAAATGCAATTAATTAAGG 600
DB 541 GAAATTTATTTATGCTTACGATATGTCAGAGCTGCAAAATGCAATTAATTAAGG 600

QY 601 GACGAGTTAATATATTAAGAAATGAGGAGCTAGTGTGCCACCGTTGATCCAGGATCA 660
DB 601 GACGAGTTAATATATTAAGAAATGAGGAGCTAGTGTGCCACCGTTGATCCAGGATCA 660
QY 661 GGGAGAACTGATTTGTAAAGCGGTTTAAAGGAAATTAAGAGATATCTAATATTGT 720
DB 661 GGGAGAACTGATTTGTAAAGCGGTTTAAAGGAAATTAAGAGATATCTAATATTGT 720
QY 721 GTAGGTTGATTAACAAGGTTTAAATCATCAATGACAGCGGGTCAAGTCTGAAGTT 780
DB 721 GTAGGTTGATTAACAAGGTTTAAATCATCAATGACAGCGGGTCAAGTCTGAAGTT 780
QY 781 TGGTGAATTTAATTAATTTTGTGAGAAATGAGCTGGCGGTATGGAATTTATTTGCT 840
DB 781 TGGTGAATTTAATTAATTTTGTGAGAAATGAGCTGGCGGTATGGAATTTATTTGCT 840
QY 841 ATATTTCCAACTTAATGATTTGAAAAATATCCATTAGCAACAAGTATGATTAAGCTAGG 900
DB 841 ATATTTCCAACTTAATGATTTGAAAAATATCCATTAGCAACAAGTATGATTAAGCTAGG 900
QY 901 GAAATTTATACGATTCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACGTTTCTT 960
DB 901 GAAATTTATACGATTCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACGTTTCTT 960
QY 961 AGCTTTAATTTGGTTGAAGCAAAATGGAACACGGGACCTGGTTAGTTACTTGGCTTCA 1020
DB 961 AGCTTTAATTTGGTTGAAGCAAAATGGAACACGGGACCTGGTTAGTTACTTGGCTTCA 1020
QY 1021 GCTATGATATATATATGATCATTTATTAATCTTCACTGTTGTTATCTTATAGTGGTGGG 1080
DB 1021 GCTATGATATATATATGATCATTTATTAATCTTCACTGTTGTTATCTTATAGTGGTGGG 1080
QY 1081 GGAATCTGTCATTAATGAAAGACTTCAAAAGGTAACGGTCTTTTCAACGATATGCTGGA 1140
DB 1081 GGAATCTGTCATTAATGAAAGACTTCAAAAGGTAACGGTCTTTTCAACGATATGCTGGA 1140
QY 1141 ACTAGAGATTAATTAACCGTAATTTATTTTGGCAATACCGATATATTTAAATTTAT 1200
DB 1141 ACTAGAGATTAATTAACCGTAATTTATTTTGGCAATACCGATATATTTAAATTTAT 1200
QY 1201 TCATTAGCTAGATATGCAATGCAACCGTTTGTGGGATTCATATCCAGCGATCTTGT 1260
DB 1201 TCATTAGCTAGATATGCAATGCAACCGTTTGTGGGATTCATATCCAGCGATCTTGT 1260
QY 1261 TCAAGTGCAGAAATTTTTCGACAAACCTAAATACCTTCTGTATGAGGTAAACAGTTCT 1320
DB 1261 TCAAGTGCAGAAATTTTTCGACAAACCTAAATACCTTCTGTATGAGGTAAACAGTTCT 1320
QY 1321 GGGTACTCACAACAATGGAATCTGTGTTACAGGATTAATTAAGGATCTACACCTAGT 1380
DB 1321 GGGTACTCACAACAATGGAATCTGTGTTACAGGATTAATTAAGGATCTACACCTAGT 1380
QY 1381 CGTACAAATTAATCTCATAGATTATCAATGCGGATGTTCAAATGAAACCTCCAGA 1440
DB 1381 CGTACAAATTAATCTCATAGATTATCAATGCGGATGTTCAAATGAAACCTCCAGA 1440
QY 1441 GTTAAAGTATTTGGTTGACACATCAAGTAAAGTAAAGAAATGCAATTTATCCAGAT 1500
DB 1441 GTTAAAGTATTTGGTTGACACATCAAGTAAAGTAAAGAAATGCAATTTATCCAGAT 1500
QY 1501 AAAATTAAGCAAAATTCGCACTAAAGCTTTTGCCTACAGAGAGGTACAGATATGGA 1560
DB 1501 AAAATTAAGCAAAATTCGCACTAAAGCTTTTGCCTACAGAGAGGTACAGATATGGA 1560
QY 1561 GAGAGTTACGTACAGCTGGGCTGTGTTATACAGAGAGAGTATGTAACGTTACTTAT 1620
DB 1561 GAGAGTTACGTACAGCTGGGCTGTGTTATACAGAGAGAGTATGTAACGTTACTTAT 1620
QY 1621 CAAGCAAGTTTAAATTAATCTTGTGACCCAGCAATTAATTAATTAATTAATTAATTA 1680
DB 1621 CAAGCAAGTTTAAATTAATCTTGTGACCCAGCAATTAATTAATTAATTAATTAATTA 1680


```
QY 1681 CTTGCTACCGGAGTGGAGGACCTGTCCTCCGATGAGAAAGATGGTCCCAAGTCT 1740
DB 1681 CTTGCTACCGGAGTGGAGGACCTGTCCTCCGATGAGAAAGATGGTCCCAAGTCT 1740
QY 1741 GTTTCAAATGCTATTTTTCGTCGACGCTACAGAGTGTATGATTCATTTGATTTG 1800
DB 1741 GTTTCAAATGCTATTTTTCGTCGACGCTACAGAGTGTATGATTCATTTGATTTG 1800
QY 1801 GACACCTTACTTACTTATCAATTAATCAATCAAGTGTGAATATTAATTAATCAATCTATCT 1860
DB 1801 GACACCTTACTTACTTATCAATTAATCAATCAAGTGTGAATATTAATTAATCAATCTATCT 1860
QY 1861 GGTACACACCTTATTTGTCGAAAGTGAATTTATCCCAATGACATCCCAATTTGAAAA 1920
DB 1861 GGTACACACCTTATTTGTCGAAAGTGAATTTATCCCAATGACATCCCAATTTGAAAA 1920
QY 1921 TGTACGAAATGTCAATTCGAAGAGACATATGATGTGAAGAGTACATCTTGAAA 1980
DB 1921 TGTACGAAATGTCAATTCGAAGAGACATATGATGTGAAGAGTACATCTTGAAA 1980
QY 1981 ACAAAGAAAGAGATTTGTAATGATTTATTTATCAATTTAA 2019
DB 1981 ACAAAGAAAGAGATTTGTAATGATTTATTTATCAATTTAA 2019

RESULT 2
ADR89413 standard; cDNA; 2145 BP.
AC ADR89413;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 full length coding sequence.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KM expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 127..2145
FT /*tag= a
FT /product= "AXMI-008"
FT /transl_except= pos:127..129, aa:Met
XX
PN MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004MO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781879.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargiss T, Koziej MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89415.
```

```
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 25; 178bp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2145 BP; 710 A; 338 C; 441 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2019; DB 13; Length 2145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAAAAATATGATTTCTTATCAAAATATCAATATGATGATTTGATGTTCCCG 60
DB 127 GTGAAAAATATGATTTCTTATCAAAATATCAATATGATGATTTGATGTTCCCG 186
QY 61 AATPACAAATATATGTCMAACAGATATCTTTTGCAAGAGATCCAAATATATTTCTATT 120
DB 187 AATPACAAATATATGTCMAACAGATATCTTTTGCAAGAGATCCAAATATATTTCTATT 246
QY 121 AACCTGACCCCTTGTGCGGAAAGCCATGCGAAGATACGTGGATCACTCTCGATATA 180
DB 247 AACCTGACCCCTTGTGCGGAAAGCCATGCGAAGATACGTGGATCACTCTCGATATA 306
QY 181 GTAACATTTGGGACATCTCTTATTAATTTCTTGCTAAGCCGTTAAGGTAATTCCT 240
DB 307 GTAACATTTGGGACATCTCTTATTAATTTCTTGCTAAGCCGTTAAGGTAATTCCT 366
QY 241 GTAATATTTTCAATATATTAACAATCTCATTCGTCCTGTCATCTGTGGACGACTT 300
DB 367 GTAATATTTTCAATATATTAACAATCTCATTCGTCCTGTCATCTGTGGACGACTT 426
QY 301 TCTATATGTGATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGCGTTAAGTGAC 360
DB 427 TCTATATGTGATTTAGTATCTATTAATTCGTAAGAGGTAGACGAGCGTTAAGTGAC 486
QY 361 GGGGTTGCAATTTTGGGTTGAATGACGCTTATCAAAATATTAATCTTCAATTACTT 420
DB 487 GGGGTTGCAATTTTGGGTTGAATGACGCTTATCAAAATATTAATCTTCAATTACTT 546
QY 421 GAGGATTTGCTTACAGTAAATCAATCTTAAATCTTCTGTCGATGTTAAACAGTTC 480
DB 547 GAGGATTTGCTTACAGTAAATCAATCTTAAATCTTCTGTCGATGTTAAACAGTTC 606
QY 481 CAAAGCAGGGAAGAGATTTCACTAACTTTTACGAGGTCATTTATCAAGCAGAAAGCT 540
DB 607 CAAAGCAGGGAAGAGATTTCACTAACTTTTACGAGGTCATTTATCAAGCAGAAAGCT 666
QY 541 GAAATTTTATTTATTTGCTTACGATATGTCAGAGCTGCAATGGAATTAATTAATTAAG 600
DB 667 GAAATTTTATTTATTTGCTTACGATATGTCAGAGCTGCAATGGAATTAATTAATTAAG 726
QY 601 GACGAGTTAAATATATATATATATATATATATATATATATATATATATATATATAT 660
DB 727 GACGAGTTAAATATATATATATATATATATATATATATATATATATATATATATAT 786
QY 661 GGAAGAACTGATTTGTAAGAGCGGTTAAAGCGAATAAAGATATATATATATATAT 720
```

```
Db 787 GGGAGACGATTTGTAAACGAGCGGTTAAAGCGAAATTAAGATTAATTAATTTG 846
Qy 721 GTRAGGTGTATTAACAAGGTTTAAATCAGATTAAGACGCGGGTCAAGTCTGAAGT 780
Db 847 GTAGGGTGTATTAACAAGGTTTAAATCAGATTAAGACGCGGGTCAAGTCTGAAGT 906
Qy 781 TGGTCAAAATTTAATAATTTGTAGAGAAATGACGTTGGCGGTATTTGATATTTGCT 840
Db 907 TGGTCAAAATTTAATAATTTGTAGAGAAATGACGTTGGCGGTATTTGATATTTGCT 966
Qy 841 AATATTTCAACTTATGATTTTGAATAATATCCATTGCAACAAGTATGATTAAGTCTG 900
Db 967 AATATTTCAACTTATGATTTTGAATAATATCCATTGCAACAAGTATGATTAAGTCTG 1026
Qy 901 GAAATTTATACAGATCCAGTGGGATTTTCAGGGGAAATTTATGTTGGGAACGTTT 960
Db 1027 GAAATTTATACAGATCCAGTGGGATTTTCAGGGGAAATTTATGTTGGGAACGTTT 1086
Qy 961 AGCTTAATTTGGGTAGAGCAAAATGGAACGCGGGAACCTGGTTAGTTAAGTCTGCA 1020
Db 1087 AGCTTAATTTGGGTAGAGCAAAATGGAACGCGGGAACCTGGTTAGTTAAGTCTGCA 1146
Qy 1021 GCTATAGATATATATATAGTCAATTTCTATTAATCTTCAAGCTTGGTTATCTT 1080
Db 1147 GCTATAGATATATATAGTCAATTTCTATTAATCTTCAAGCTTGGTTATCTT 1206
Qy 1081 GGAACCTGTCATATGATTAAGACCTTCAACAAAGGTTAAGGTCCTTTCAAGTATG 1140
Db 1207 GGAACCTGTCATATGATTAAGACCTTCAACAAAGGTTAAGGTCCTTTCAAGTATG 1266
Qy 1141 ACTACAGATTAATATATATATATATATATTTTGGCAATATCGATTAATTAATTA 1200
Db 1267 ACTACAGATTAATATATATATATATATATTTTGGCAATATCGATTAATTAATTA 1326
Qy 1201 TCATTAAGTATGATATGCAATGCAACCGTTGTTGGGATTTCAATCCACGCACT 1260
Db 1327 TCATTAAGTATGATATGCAATGCAACCGTTGTTGGGATTTCAATCCACGCACT 1386
Qy 1261 TCACGTCGCAAAATTTTTCGCAACACATTAATCTTCTGATAGAGTTAAACAGT 1320
Db 1387 TCACGTCGCAAAATTTTTCGCAACACATTAATCTTCTGATAGAGTTAAACAGT 1446
Qy 1321 GGGTACTCAGACAAATTTGATGATCTGTGTACAGATTAATTAAGATCTACCACT 1380
Db 1447 GGGTACTCAGACAAATTTGATGATCTGTGTACAGATTAATTAAGATCTACCACT 1506
Qy 1381 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGGCAATGTTCAAAATGAA 1440
Db 1507 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGGCAATGTTCAAAATGAA 1566
Qy 1441 GTTAAAGTATTTGGTGGGACACATACAGATTAAGAAAAATATGAATTTTCCAG 1500
Db 1567 GTTAAAGTATTTGGTGGGACACATACAGATTAAGAAAAATATGAATTTTCCAG 1626
Qy 1501 AAAATATCCCAAAATTTCTGAGTAAGAAAGCTTTTGGCCCTACACAGATTAAG 1560
Db 1627 AAAATATCCCAAAATTTCTGAGTAAGAAAGCTTTTGGCCCTACACAGATTAAG 1686
Qy 1561 GGAAGTTACGTCACAGCTGGGCTGTATATACAGAGAGATGATTAACGTTACCT 1620
Db 1687 GGAAGTTACGTCACAGCTGGGCTGTATATACAGAGAGATGATTAACGTTACCT 1746
Qy 1621 CAAGCAAGTTTAAATATAGCTTTAATCTTGCACCAACGAATTAATTAACGTT 1680
Db 1747 CAAGCAAGTTTAAATATAGCTTTAATCTTGCACCAACGAATTAATTAACGTT 1806
Qy 1681 CTTCGCTACGCGAGTGAAGACCTGGTCCGTTCCGATGAGAAAGATGTCGCCAAGT 1740
Db 1807 CTTCGCTACGCGAGTGAAGACCTGGTCCGTTCCGATGAGAAAGATGTCGCCAAGT 1866
Qy 1741 GTTCAAAATGCTAATTTTCTGCTCAGCTACAGAGTGGCTATATGTTCAATTT 1800
```

```
Db 1867 GTTCAAAATGCTAATTTTCTGCTCAGCTACAGAGTGGCTATATGTTCAATTT 1926
Qy 1801 GACACCTTAGTTACTATCAATTAATCAATCAGGTGTTGAAATATTAATTAATTA 1860
Db 1927 GACACCTTAGTTACTATCAATTAATCAATCAGGTGTTGAAATATTAATTAAT 1986
Qy 1861 GGTATCCACCTTATTTGTGACAAAGTCGAATTTATCCCAATTTGACATCCAA 1920
Db 1987 GGTATCCACCTTATTTGTGACAAAGTCGAATTTATCCCAATTTGACATCCAA 2046
Qy 1921 TGTAGCAAAATGTCATTTCCAGAGACATATGTAGTGTGAAGATCAATCTTGA 1980
Db 2047 TGTAGCAAAATGTCATTTCCAGAGACATATGTAGTGTGAAGATCAATCTTGA 2106
Qy 1981 AAAAAAAAAAGATTTGTAATATGTTATTTATCAATTA 2019
Db 2107 AAAAAAAAAAGATTTGTAATATGTTATTTATCAATTA 2145

RESULT 3
ADR89416 standard; cDNA; 2010 BP.
ID ADR89416
XX
AC ADR89416;
XX
DT 18-NOV-2004 (first entry)
XX
DE AKMT-008 alternative start site coding sequence.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
XX expression cassette; transformation; transgenic; plant; bacteria;
XX lepidoptera; coleoptera; pest; pesticide; resistance;
XX pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2010
FT FT /tag= a
FT FT /product= "Alternative AKMT-008"
XX
PN MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
P2 20-FEB-2004; 2004MO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782147.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
XX
XX P-PSDB; ADR89417.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 28; 178bp; English.
XX
```

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SQ Sequence 2010 BP; 657 A; 324 C; 417 G; 612 T; 0 U; 0 Other;

Query Match	99.6%;	Score 2010;	DB 13;	Length 2010;
Post Total	100.0%	Post Val	0	

Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	10	ATGAATCTCTATCAAAAATAAATAATCAATCAATGAAATTCGAGATGGTTCCTCCGAAATACGA	69
Db	1	ATGAATCTCTATCAAAAATCAAAATBAATATGTAATTCGAGATGGTTCCTCCGAAATACGA	60
OY	70	AATATGTCAAA CAGATATCTTTTGGCAAAAGATCCAAATATATYTTCTATTAACTGTGAC	129
Db	61	AATATGTCAAA CAGATATCTTTTGGCAAAAGATCCAAATATATYTTCTATTAACTGTGAC	120
OY	130	GCTTGTCAGGGAAAGGCCATGCGCAGATACGTGGGAATCAGTCTCGGATATATGTAACTATTT	189
Db	121	GCTTGTCAGGGAAAGGCCATGCGCAGATACGTGGGAGATCAGTCTCGGATATATGTAACTATTT	180
OY	190	GGGACATACCTTATACAAATTCCTGTGTACAA CCGGATATAGGAGAAATTCCTGTATATTT	249
Db	181	GGGACATACCTTATACAAATTCCTGTGTACAA CCGGATATAGGAGAAATTCCTGTATATTT	240
OY	250	TCAATTAATAAACAACATCATTCGCTCTCTGGTCACATCTGTGGCAGCACTTCTATATGT	309
Db	241	TCAATTAATAAACAACATCATTCGCTCTCTGGTCACATCTGTGGCAGCACTTCTATATGT	300
OY	310	GATTTAGTATCTATATATTCGTAAAGAGGTAGACGAGACGCTGTAAAGTACGCGGGTTCGA	369
Db	301	GATTTAGTATCTATATATTCGTAAAGAGGTAGACGAGACGCTGTAAAGTACGCGGGTTCGA	360
OY	370	GATTTTGGGGGTGAAATGACCTGCTTATCAAGATTATATCTTCATATCTTGAAGATTGG	429
Db	361	GATTTTGGGGGTGAAATGACCTGCTTATCAAGATTATATCTTCATATCTTGAAGATTGG	420
OY	430	CTTACAGATTAATCAAAATCTCTAAAAAACTTGGCTGAGTATTAACAGTTCCAAAGCACGG	489
Db	421	CTTACAGATTAATCAAAATCTCTAAAAAACTTGGCTGAGTATTAACAGTTCCAAAGCACGG	480
OY	490	GAAGAAATYTTCACTAAACTTTTAGCAGGGTCATTATCAAGACAAAGCTGAATATATTA	549
Db	481	GAAGAAATYTTCACTAAACTTTTAGCAGGGTCATTATCAAGACAAAGCTGAATATATTA	540
OY	550	TTATTTGCTTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTACTATTAAGGACGCAGTT	609
Db	541	TTATTTGCTTACGTATGTGCAAGCTGCAAAATGTGCAATTTATTACTATTAAGGACGCAGTT	600
OY	610	AAATATTAATAAAGAATGGGACCTAGTGTGTCACACGGTGTATCCAGGGGTCAAGGAGAACT	669
Db	601	AAATATTAATAAAGAATGGGACCTAGTGTGTCCACCGTTGTATCCAGGGGTCAAGGAGAACT	660
OY	670	GATTGTAAACGAGCGGTTAAAAACGAAATTAAGAAGTATACTAATTAATTTGTAGAGGTGG	729
Db	661	GATTGTAAACGAGCGGTTAAAAACGAAATTAAGAAGTATACTAATTAATTTGTAGAGGTGG	720
OY	730	TTATAACAAGGCTTTAGATCAGATTAAGACAGCGCGGTACAAAGTCTCGAAAGTTTGGTTCGAA	789
Db	721	TTATAACAAGGCTTTAGATCAGATTAAGACAGCGCGGTACAAAGTCTCGAAAGTTTGGTTCGAA	780

```
Db      1861 CTTATTGTTGCAAGGATTCATTCACATTCACAAATTTGAAAAATGTACGAAA 1920
Qy      1930 TGTCAATTCGAAGACACATATGTAGATGTGAAGAGATACAAATCCTTGAAACAAAAAA 1989
Db      1921 TGTCAATTCGAAGACACATATGTAGATGTGAAGAGATACAAATCCTTGAAACAAAAAA 1980
Qy      1990 GAGATTGTAAATAGTTATTTATTCATTA 2019
Db      1981 GAGATTGTAAATAGTTATTTATTCATTA 2010

RESULT 4
ADR89401
ID      ADR89401 standard; cDNA; 2082 BP.
XX
AC      ADR89401;
XX
DT      18-NOV-2004 (first entry)
XX
DE      AXMI-008 coding sequence.
XX
KW      sei; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW      expression cassette; transformation; transgenic; plant; bacteria;
KW      lepidoptera; coleoptera; pest; pesticide; resistance;
KW      pesticidal activity.
XX
OS      Bacillus thuringiensis.
XX
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      1..2082
FT      /*tag= a
FT      /product= "AXMI-008"
FT      /transl_except= pos:1..3, aa:Met

MO2004074462-A2.
XX
PD      02-SEP-2004.
XX
PF      20-FEB-2004; 2004MO-US005829.
XX
PR      20-FEB-2003; 2003US-0448632P.
XX
PR      20-FEB-2003; 2003US-0448633P.
XX
PR      20-FEB-2003; 2003US-0448797P.
XX
PR      20-FEB-2003; 2003US-0448806P.
XX
PR      20-FEB-2003; 2003US-0448810P.
XX
PR      20-FEB-2003; 2003US-0448812P.
XX
PR      19-FEB-2004; 2004US-00781979.
XX
PR      19-FEB-2004; 2004US-00782020.
XX
PR      19-FEB-2004; 2004US-00782096.
XX
PR      19-FEB-2004; 2004US-00782141.
XX
PR      19-FEB-2004; 2004US-00782570.
XX
PR      19-FEB-2004; 2004US-00783417.
XX
PA      (ATHE-) ATHENIX CORP.
XX
PI      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B,
XX
DR      WPI; 2004-635574/61.
XX
DR      P-PSDB; ADR89402.
XX
PT      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT      and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT      for producing organisms with pesticide resistance.
XX
PS      Claim 1; SEQ ID NO 13; 178bp; English.
XX
CC      This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC      endotoxin coding sequences of the invention have alternative start
CC      codons, producing more than one protein from a single open reading frame.
CC      The nucleic acid sequences of the invention are useful in DNA constructs
CC      or expression cassettes for transformation and expression in plants and
CC      bacteria. The nucleic acids and corresponding polypeptides are useful for
```

```
CC      killing lepidopteran or coleopteran pests. Compositions containing the
CC      delta-endotoxins of the invention, and methods for their production, are
CC      useful for the production of organisms with pesticide resistance.
CC      specifically bacteria and plants. These organisms are useful for
CC      generating altered or improved delta-endotoxin or delta-endotoxin-
CC      associated proteins that have pesticidal activity, or for detecting the
CC      presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC      nucleic acids in products or organisms.
SQ      Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;
Query Match      37.0%; Score 747.2; DB 13; Length 2082;
Best Local Similarity 69.8%; Pred. No. 1.7e-179;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;
Qy      1 GTGAAAAATATGATTTCTTATCAAAATACAAATGAAATGAAATTCGTGATGTCCTCCG 60
Db      1 GTGAAAAAGATGATTCATATCAAAATGAAATGAAATGAAATGAAATTCGTGATGTCCTCCG 60
Qy      61 AATTAACAAATATGTCACACAGATATCCTTTTGCAAGAGATCCAAATATATTTCTATT 120
Db      61 AATTAACAAATATGCGCAACACAGATATCCTTTTGCAAAATATCGGATATGCTACTATG 120
Qy      121 AACCTGACGCTTGTCAGGGAAGCCCATGCAAGATACGTGGAAATCACTCGATATA 180
Db      121 TCTTGAATGATTTGTCAGGGAATCATGGAATGAAATTTGGGAATCACTCGAAACGATA 180
Qy      181 GTTAACTTTGGACATACCTTTATACAAATCTTGCTGTAACCCGGATAGTGAATTCCT 240
Db      181 ACAAGTATGGAGATTAATCTTATAGAGTTTGATAGAACTTAATTTGGGTGGAATTAAT 240
Qy      241 GTTAAATTTTCAATATAAACAACATTCCTCGCTCTGTCATATCTGTGGACAGACTT 300
Db      241 ACACTTTTCAATATATAGAAACAACTTAATTCGACTAATCGTCAAACTGTGACACACTT 300
Qy      301 TCTATATGATTTAGTATCTATTAATTCGTAAGAGTGAAGACAGACCTGTTAAGTAC 360
Db      301 TCTATATGATTTATATCTATTAATTCGTAAGAGTGAAGACAGATGCTTTAAGTAT 360
Qy      361 GGGGTTCAGATTTTGAAGGTGAATGACTGCTTATCAAGATTTATCTTATTCTT 420
Db      361 GCGATTGCAGATTTTGAAGGTGAATTTGAATAATTAAGAGATTAATCTTCTTATCTT 420
Qy      421 GAGGATTTGGCTTACG-----ATAATCAATCTTAAAACTTGCTGAC 465
Db      421 GGGGCTTGGCTTAAAGACGTTAAACCTTCAAAAGACAAATTAATCTGATATGACAA 480
Qy      466 GTAGTTAAACAGTTCACACGAGGAAGAAATTTCACTAACTTTAGCAGGTCATTA 525
Db      481 TTAGTTATTTATTTAACTTTCAAGAAAGATTTCAATGAATTTCTAGAGGGTCATTG 540
Qy      526 TCAAGACAAAAGCTGAATATTTATTTGCTTACGTATGTGCAAGCTGCAAATGTGCAT 585
Db      541 TCAAGAAACAAATGCTCAAGATTTGTTATTAATCTTTGCAACAACTGCAAATGTGCAG 600
Qy      586 TTATTACTATTAAAGGACGCTTAATTAATTAATAAAGAAATGGGGACTAGTGTCACCG 645
Db      601 TTAATTAATTAAGGATGAGTTCATATTAAGACAAATGTTTCCATTTTGTAGTGA 660
Qy      646 TTGTATCCAGGCTCAGGAGAA-----CTGATGT 675
Db      661 GAGAAATGTAAGTCGGAATTTAATATCACTTAACAGTGTGATTTACCGGTGATTAAC 720
Qy      676 AACGACGGTGAAGCGAAATTAAGAGTATCAATTAATTTGTAGGGTGTATAAC 735
Db      721 TATGACCGATTAATAAGCAAAACGCGAGATATCAATTAATTTGTTATATGATCAG 780
Qy      736 AAGGTTTGAATGATTAAGACAGCGGGGTACAAAGCTGCAAGTTTGTGCAATTTAAT 795
Db      781 GTAGTTTAATATAGTAAACAGGGGGGACAGGGCTGACACTTGGTCAATTTAAT 840
Qy      796 AATTTTCGTAGAAATGACGTTGGCGTATTTGATTTATTTGCTAATTTTCCAACTTAAT 855
```

```

Db      841 AATTGTGTAGAGAAATGACGTGGCGGTATTTGATATATTCGATATTTCCAACTTAT 900
Qy      856 GATTTTGAAAAATATTCATTAGCAACAAGTGTAGAGTTAACTAGAGAAATTTATACAGT 915
Db      901 GATTTTGAGAAATATTCATTAGCAACAAGTGTAGAGTTAACTAGAGAAATTTATACAGT 960
Qy      916 CCAGTGGGATTTGAGGGGAAATTAAGTTGGGAACGGTTT-----TTAGCTTAAAT 969
Db      961 GCAGTGGGATTTGAGGGGAAATTAAGTTGGGAACGGTTT-----TTAGCTTAAAT 1020
Qy      970 TCGGTAGAGCAATAGGAAACACGGGACCTGTGTAGTTACTTGGCTTCAAGTATATAGAT 1029
Db      1021 GGGTTAGAGGCTATATGAAACACGGGACCTGTGTAGTTACTTGGCTTCAAGTATATAGAT 1080
Qy      1030 ATATATAGTCAATCTTATTAATCTTCAAGTTGGTTATCTTACGTGGGGGGAACTCGT 1089
Db      1081 ATATATATAGTATATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGAACCTGT 1131
Qy      1090 CATATAGAACTTCAACAAAGGTTAAGGTCCTTTTCAACGTATGTCTGAACTACAGAT 1149
Db      1132 CATATAGAACTTCAACAAAGGTTAAGGTCCTTTTCAACGTATGTCTGAACTACAGAT 1191
Qy      1150 AATAATCAGCTAATATTTATTTGGCAATACCGATATATTTAAATTAATTTCAATAGCT 1209
Db      1192 AATGATCTAGCTAATATTTATTTGCAATGCCATGTATATTAATTAATTTCAATAGCT 1251
Qy      1210 AGATATGCAATGCAACCGTTTGTGGTATTCATCCACGGCACTTGTGTTTCACTGCA 1269
Db      1252 A---TCATGAACCTAGTAGAGAGAACATACCGCTAGACAGATACGTTTCAAAAGCA 1308
Qy      1270 GAATTTTTCGCAACAACCTAATATCTTCTGTATAGAGTTAAACAGTTCTGGG---TAC 1326
Db      1309 GATTTTGTGGGGTAGGGGGACCTGATTTAAATATATGATGACGGTAAATTAATGAGCTTAC 1368
Qy      1327 TCACAGCAATGTAATCTGTGTACCAAGTATTAATAGATCTACCAACCTAGTCGTACA 1386
Db      1369 AGATGCAATGTAATCTAGCTTCCACTTGT-----ATTGCACTTAATGAGTGTAGA 1422
Qy      1387 AATTACTCTCATAGATTATCAAAATGCGCAATGTGTTCAAAATGAAACCTCCAGAGTTAC 1446
Db      1423 GGAACCTCTCATATATTAATTAATGCGCAATGTGTTCAAAATGAAACCTCCAGAGTTAC 1482
Qy      1447 GTATTTGGTGGACACTACATGATATGAAAAAGATATATGCAATTTATCCAGATTAAT 1506
Db      1483 GTATATGTTGGACACTACATGATTAATGAAAAAGTAAATATTAATGAAGCAATCAAT 1542
Qy      1507 ACCGAATTCCTGTCAGTAAAGCTTTTGCCCTACACAGAGGTACAGATATGACGAGGT 1566
Db      1543 ACACAAATACCGGCGGTGAAGAGTTATTAATCTCAAAATTAATCTTGAATGCTATACC 1602
Qy      1567 TACGTCAACAGCTGGGCT 1584
Db      1603 TATGTATTAATAAGGCACT 1620

```

RESULT 5
 ADR89400 ID ADR89400 standard; cDNA; 5980 BP.

XX ADR89400;

DT 18-NOV-2004 (first entry)

XX AXMI-008 full length coding sequence.

XX ss: gene: delta-endotoxin; delta-endotoxin associate polypeptide;
 KM expression cassette; transformation; transgenic; plant; bacteria;
 KM lepidoptera; coleoptera; pest; pesticide; resistance;
 XX pesticial activity.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers

```

FT      CDS      168..2249
FT      /*tag= a
FT      /product= "AXMI-008"
FT      /transl_except= pos:168..170, aa:Met
XX      W02004074462-A2.
PD      02-SEP-2004.
XX      20-FEB-2004; 2004MO-US005829.
PF      20-FEB-2003; 2003US-0448632P.
PR      20-FEB-2003; 2003US-0448633P.
PR      20-FEB-2003; 2003US-0448797P.
PR      20-FEB-2003; 2003US-0448806P.
PR      20-FEB-2003; 2003US-0448810P.
PR      20-FEB-2003; 2003US-0448812P.
PR      19-FEB-2004; 2004US-00781979.
PR      19-FEB-2004; 2004US-00782020.
PR      19-FEB-2004; 2004US-00782096.
PR      19-FEB-2004; 2004US-00782141.
PR      19-FEB-2004; 2004US-00782570.
PR      19-FEB-2004; 2004US-00783417.
XX      (ATHE-) ATHENIX CORP.
XX      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
PI      WPI; 2004-635574/61.
DR      P-PSDB; ADR89402.
XX      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT      and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT      for producing organisms with pesticide resistance.
XX      Claim 1; SEQ ID NO 12; 178bp; English.
XX      This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC      endotoxin coding sequences of the invention have alternative start
CC      codons, producing more than one protein from a single open reading frame.
CC      The nucleic acid sequences of the invention are useful in DNA constructs
CC      or expression cassettes for transformation and expression in plants and
CC      bacteria. The nucleic acids and corresponding polypeptides are useful for
CC      killing lepidopteran or coleopteran pests. Compositions containing the
CC      delta-endotoxins of the invention, and methods for their production, are
CC      useful for the production of organisms with pesticide resistance.
CC      specifically bacteria and plants. These organisms are useful for
CC      generating altered or improved delta-endotoxin or delta-endotoxin-
CC      associated proteins that have pesticidal activity, or for detecting the
CC      presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC      nucleic acids in products or organisms.
XX      Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;
SQ

```

Query Match 37.0%; Score 747.2; DB 13; Length 5980;
 Best Local Similarity 69.8%; Pred. No. 2,4e-179;
 Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

```

Qy      1 GTGAAAAATATGAAATCTTATCAAAATGAAATATGAAATTTCTGATGTTCCCG 60
Db      168 GTGAAAAAGATGATCATATCAAAATGAAATATGAAATATGAAATCTCATCG 227
Qy      61 AATACACAAATATGTCAAACAGATATCTTTGCAAAAGATCAATATATTTCTATT 120
Db      228 AATACACAAATATGCGCAACAGATATCTTTGCAAAATATGCGATATGTCTACTATG 287
Qy      121 AACCTGACGCTTGTGAGGAGCGCATGCGCAAGATACGTGGAATCACTGGAATAT 180
Db      288 TCTTGGAATGATGTGACGGAATCTCATGGAATGGAATTTGGGAATCAGCGAAAGAT 347
Qy      181 GTAACATTTGGGACATACCTTATATCAAAATCTTGTGTAACCGCGTATAGTGGAATTC 240
Db      348 ACBAATTTGGGATTAATCTTATAGAGTTGTGATGAAACCTTGTGGTGGGAATTAAT 407

```

QY 241 GATAATTTTCAATATTAACAACTCATTCGGCTTGGTCAATCTGGGAGACCTT 300
 DB 408 AACTATTTATCAATTAATAGAAAATCTAATTCGACATTAATGTAACCTGGTGACGACT 467
 QY 301 TCTATAATGATTTAGTATCTATTAATTCGTAAAGAGTAGACGAGCGGTAACTGAC 360
 DB 468 TCTATATGATTTATTTATCTATTAATTCGTAAAGAGTAGCCATAGTGTATTAAGTAT 527
 QY 361 GGGGTTCAGATTTTGAAGGTGAATGACCTGATTCAGATTTATCTTCACTTATCTT 420
 DB 528 GCGATTCAGATTTTGAAGGTGAATTAAGAGATTAATCTTCTTATCTT 587
 QY 421 GAGATTTGGCTTACAG-----ATTAATCAAAATCTTAAAAAATCTTGGTAC 465
 DB 588 GGGGCTTGGCTTAAAGCGTAAACCACTTCAAAAGCAATTAATCTGATTCGACAA 647
 QY 466 GTATGTTAAACAGTTTCAAGACGGAAGAAAGATTTCCTAACTTTTAGCAGGGTCACTA 525
 DB 648 TTATGTTATTAATTTTAACTTTTCAGAAAGAGATTTCAATGAATTCAGAGGGGTCACTG 707
 QY 526 TCAAGACAGAAAGCTGAAATATTTATTTGCTTACGATGTCAGAGCTGCAATGTGCAT 585
 DB 708 TCAAGAAACAGTCTCAAGATTTGTTATTACTTATTCAGACAGCTGCAAAATGTGCAG 767
 QY 586 TTATTAATTAAGGACGAGTTAAATATTAATAAAAGATGGGGAATGATGTCCACCG 645
 DB 768 TTATTAATTAAGGATGACGATTCATTAATTAAGACAAATGTCCATTTTGAATGCA 827
 QY 646 TTGTATTCAGGGTCAAGGAGAA-----CTGATTTG 675
 DB 828 GAGAAATGTAAGATCGGAATTAATATATCACTAACAGTGTGTGATTTTACCGGTGATAC 887
 QY 676 AAGAGCGGTAAAGGAAATTAAGAAATATTAATTAATTTGTGAGGTGTGATTAAC 735
 DB 888 TATGAGGATTAATAATGCAAAACGGCAGATATTAACAAATTAATTTATTTGATTCAG 947
 QY 736 AAGGTTTATGATGATTAAGACAGCGGTGACAAAGTCTGAAGTTTGTGCAATTAAT 795
 DB 948 GTAGGTTTAAATCAGTAAACAGCGGGGACAGTGCTGACACTTGTGCAATTTAT 1007
 QY 796 AAATTTGATGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATTTTCCAACTTAT 855
 DB 1008 AAATTTGATGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATTTTCCAACTTAT 1067
 QY 856 GATTTTGAATAATTCATTAAGCAACAGTGTAGATTAATCTAGGAAATTTTATACAGAT 915
 DB 1068 GATTTTGAATAATTCATTAAGCAACAGTGTAGATTAATCTAGGAAATTTTATACAGAT 1127
 QY 916 CCAATGGGATTAATCAAGGGGAAATTAATGTTGGGAACGTTTT-----TTAGCTTAAAT 969
 DB 1128 GCAATGGGATTAATCAAGGGGAAATTAATGTTGGTACGGAATTTGCTTAAATCTTTTAAAT 1187
 QY 970 TCGGTAGAAACAAATGAGAACAGCGGACCTGTTTATTAATTTGCTTCAAGCTATTAAT 1029
 DB 1188 GGGTTAGAGCTAATGAGAACAGCGGACCTGTTTATTAATTTGCTTCAAGCTAATTAAT 1247
 QY 1030 ATATTAATGATCTATTAATCTTCACTTGGTTATCTTATGCTGCGGGGGAATCTCGT 1089
 DB 1248 ATATTAATGATGATGTT-----TCAGATTAATTTTCCGCGCTGGGATGAGAACTCGT 1298
 QY 1090 CATTATGAAGACTTCAAAAGGTAACGATGCTTTTCAAGATTAATGTCGAGACTAGAGAT 1149
 DB 1299 CATTATGAAGACTTCAAAAGGTAACGATGCTTTTCAAGATTAATGTCGAGACTAGAGAT 1358
 QY 1150 AATTAATCAGTAATTAATTTTGGCAATACCGATTAATTTAAATTAATTTTATTAAGCT 1209
 DB 1359 AATGAATCAGTAATTAATTTTCAAGATTCGATTAATTAATTAATTTTATTAAGCT 1418
 QY 1210 AGATATGCAATGCAACCGTTTGTGGTATTAATCCACGCGATCTTGTTCACGTCGA 1269
 DB 1419 A--TCATGAACCTAGTAGAGAGACTACCGCTAGACAGATTAATCGTTTCAAAAGGCA 1475

QY 1270 GAATTTTCCGACAACTAAATACTTCTGATAGAGTAAACAGTTCTGG--TAC 1326
 DB 1476 GAATTTTGGAGTATGGGGGACCTGATTTAAATTAATGATGAGTAAATTAATGGCTAAC 1535
 QY 1327 TCACAGACAAATGAATCTGTGTTTACAGGATTAATTAAGATCTACCACTAGTGTACA 1386
 DB 1536 AGGATGACAAATGAATCAATCAAGTTCCACTTGT-----ATTGACCTTAATGGTGTAGA 1589
 QY 1387 AATTACTCTCATATGATTTATCAAAATGCGGATGTCGAAAAAGAAACCTCCAGATTAAC 1446
 DB 1590 GGACCTCTCATATGATTTTCAAAATGCGGATGTCGAAAAAGTATGAGAACTCCAGAGTAC 1649
 QY 1447 GTATTTGTTGAGACATTAAGATTAAGAAAAAGATTAATCGAATTTATCAATTAATTT 1506
 DB 1650 GATATGTTGAGACATTAAGATTAAGAAAAAGTATTAATTAATTAATTAATTAATTAAT 1709
 QY 1507 ACGCAATTTCTGACATTAAGCTTTTGGCTTACACAGCAGGTACAGATATCAGAGAT 1566
 DB 1710 ACACAAATACCGCGGTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1769
 QY 1567 TACGTACAGCTGGGCT 1584
 DB 1770 TATGTAATTAAGGACT 1787

RESULT 6
 ADR89403
 ID ADR89403 standard; cDNA; 2073 BP.
 AC ADR89403;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 XX
 DE AXMT-008 alternative start site coding sequence.
 XX
 KW se; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key
 FT CDS 1. 2073
 FT /tag= a
 FT /product= "Alternative AXMT-008"
 XX
 PN MO2004074462-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004MO-US005829.
 XX
 PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.
 PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX
 PA (ATHE-) ATHENIX CORP.
 XX
 PI Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
 DR WPI; 2004-635574/61.
 DR P-PSDB; ADR89404.
 XX


```

DT 04-JUL-2000 (first entry)
XX Sequence encoding truncated Cry9Aa toxin.
XX
XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
XX ds.
XX
XX Synthetic.
XX Bacillus thuringiensis; ssp. galleria.
XX
XX Key Location/Qualifiers
XX CDS 17..1966
XX FT /*tag= a
XX FT /product= "Cry9Aa toxin N-terminal fragment"
XX
XX MO200011025-A1.
XX
XX 02-MAR-2000.
XX
XX 24-AUG-1999; 99MO-F1000698.
XX
XX 24-AUG-1998; 98FI-00001809.
XX
XX (UNIC-) UNICROP LTD.
XX
XX Kuvshinov V, Kanerova A, Koiyu K, Penu E;
XX
XX WPI: 2000-224660/19.
XX P-PSDB; AA183039.
XX
XX Modified synthetic DNA sequences comprise modification of the truncated
XX PT cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX PT plants.
XX
XX Claim 2, Page 55-57; 90pp; English.
XX
XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
XX CC gene of Bacillus thuringiensis ssp. galleria can be used for the
XX CC production of a unique insecticidal protein having the same properties as
XX CC the N-terminal domain of the insecticidal protein encoded by the native
XX CC cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
XX CC toxin works by binding to specific receptor molecules in the gut of
XX CC insects with consequent formation of ion channels in the epithelium. This
XX CC action leads to ion efflux and paralysis of the intestinal function.
XX CC which causes death of the insect. The synthetic DNA sequences exhibit
XX CC enhanced expression through improved mRNA processing, stability, and/or
XX CC translation providing improved tolerance against target insects. They can
XX CC be used in the production of transgenic plants capable of expressing the
XX CC N-terminal domain of the insecticidal protein encoded by the native
XX CC cry9Aa gene. They therefore have a role in pest control and crop
XX CC protection
XX
XX SQ Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;
XX
XX Query Match 8.6%; Score 174; DB 3; Length 1983;
XX Best Local Similarity 54.3%; Pred. No. 1,2e-33;
XX Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;
XX
XX QY 161 GGGAAATCAGTCTGGATATAGTAATTTGGGACATACCTTAATTCCTGTAAGC 220
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 144 GCGATGCAGCAAAAGAGACAGATCTATTTGGGCAACCATAGTCTCTTAATCAGAGC 203
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 221 CCGGTATAGGTGAATTCCTGTAATTTT-----CAATATTAACCAACTCATTCGG 214
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 204 CTTCCTTACTGATTAATTTCAATGATATAGACCTTAATAGGTAAGTCTAGAGGTA 263
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 275 CTTCGTGCAATCTGTCAGACACTTCTATATGATTTAGTATCTAATTCGTAAG 334
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 264 GTAGTGGACAAATCCATATCGATTTTGTCTATATGATCTTATATCTATTTGATTTAC 323
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 335 AGGTAGACGAGCGGTGTTAGTGACGGGTGCAATTTTGAAGGTGAATGATCGCTT 394
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX DB 324 GGGTAAGTCAGAGTGTGTTAAATGATGAGGATTCAGATTTTAATGTTCTGTAATCTTAT 383
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

QY 395 ATCAAGATTATATCTTC-----ATTATCTTGAGGATTTGGCTTACAGATA 439
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 384 ACAGAACTATTTAGAGGCTCTGATAGCTGGAATAGAAATCTTAATCTGCTTGC 443
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 440 AATCAAAATCCTAATAAACTTGTGCTGACGTAGTAAACAGTTCACAGACAGGAAGAT 499
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 444 AAGAACTCCGTACTGCTTTTAAATCCCGACTCAGAAATTTGATAGAAATTTTACC 503
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 500 TCATTAACCTTTTACAGGGTCTATTATCAAGACAGAAAGCTGAATTTATTTATG 559
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 504 GGTCTTTAAGCATGCTGCTGTTAGCTAGCAAAAATGCCAAATATTAATTAATC 563
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 560 CGTATCTGCAACCTCCAAATGTCATTTATTTCTATTAAGGACCCAGTTAATTAATA 619
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 564 CTTTTCGAGCGCTCATATTTTCCATTTATTACTACTAAGGATCTACTAGATATGCA 623
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 620 AAGAAATGGGACTAGTGTGTCCACCGTTGTATCCAGGTCAGGAGAACTGATTTGA 679
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 624 CTAAATTTGGGGCTATATACATGCTACACCTTTATATA-----ATTATCAAT 668
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 680 AGCGGTTAAAGCGAAATTAAGATATCTAATTAATTTGTGTAGGGTATTAACAAG 739
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 669 CAAAATAGTAGAGCTTATTTGAACATATATAGATTAATGCGTACATTTGTATTA 728
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 740 GTTTAGATCAGATTAAGACAGCGGGTACAGGCTGAAGTTGTGCAATTTAATTAAT 799
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 729 GTTTCAACGACTTAAGACAGAGGACATGAGCTACAGCTGTGTTAGAAATTTCAAT 788
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 800 TTGTAAGAAATGACGTTGGCGTATTTGATATTTATTTTCCAACTATGAT 859
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 789 ATCGTAGAGATGATGATTTGATTTAGATATGATGATGATTTCACTTTGATTA 848
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 860 TTGAAATATATCATTTAGCAACAAGTGTAGAGTTAATGGAATTTATACAGATCC 919
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 849 TTACTAATTAATCCCAATAGAAACAGATTTCACTGATGATGAGGTCATTTATACAGATCCAA 908
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 920 TGGGATATTCAGGGGAAATTTGTGTTGGGA 951
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 909 TTGTTTGTGATCATGTAGTGTCTTAAAGGA 940
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 8
AA293235
ID AA293235 standard; DNA; 3837 BP.
XX
XX AA293235;
XX
XX 15-SEP-2003 (revised)
XX
XX DT 04-JUL-2000 (first entry)
XX
XX Sequence encoding native Cry9Aa toxin.
XX
XX Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
XX ds.
XX
XX Bacillus thuringiensis; ssp. galleria.
XX
XX Key Location/Qualifiers
XX CDS 385..2364
XX FT /*tag= a
XX FT /product= "Cry9Aa toxin"
XX
XX MO200011025-A1.
XX
XX 02-MAR-2000.
XX
XX 24-AUG-1999; 99MO-F1000698.
XX
XX 24-AUG-1998; 98FI-00001809.
XX
XX (UNIC-) UNICROP LTD.
XX

```

PI Kuvshinov V, Kanerova A, Koiyu K, Pehu E;
 XX WPI, 2000-224660/19.
 DR P-PSDB; AAV82988.
 XX Modified synthetic DNA sequences comprise modification of the truncated
 PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in
 PT plants.
 XX Claim 10; Page 57-59; 90pp; English.
 PS
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
 CC gene of *Bacillus thuringiensis* ssp. *galleria* can be used for the
 CC production of a unique insecticidal protein having the same properties as
 CC the N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene of *Bacillus thuringiensis* ssp. *galleria*. The insecticidal
 CC toxin works by binding to specific receptor molecules in the gut of
 CC insects with consequent formation of ion channels in the epithelium. This
 CC action leads to ion efflux and paralysis of the intestinal function. This
 CC which causes death of the insect. The synthetic DNA sequences exhibit
 CC enhanced expression through improved mRNA processing, stability, and/or
 CC translation providing improved tolerance against target insects. They can
 CC be used in the production of transgenic plants capable of expressing the
 CC N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene. They therefore have a role in pest control and crop
 CC protection. (Updated on 15-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;
 Query Match 8.6%; Score 174; DB 3; Length 3837;
 Best Local Similarity 54.3%; Pred. No. 1.6e-33;
 Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;
 QY 161 GGGAAATCAGTCTCGATATATAGTAACTATGGAACATACCTTATCAATTCCTGTAGAAC 220
 DB 542 GCGATGACAGCAAGAAAGACGATATCTATGGAACACCATAGTCTCTTATCAGACAC 601
 QY 221 CCGGTATAGGTGGAATTCCTGTAAATTTT-----CAATATTAACAACATCTATTCGT 274
 DB 602 CTCTCTTACTGATTAATTAATTAATGATGATGACCTTAATGTAAGTAACTAGAGAGTA 661
 QY 275 CTTCGTGCAATCGTGGACGACACTTCTATATAGTAAATAGTATCTATATTCGTAAAG 334
 DB 662 GTAGTGAACAATCAATCAATGATTTGCTATATGATGACTTATTAATTAATGATTTAC 721
 QY 335 AGGTAGACGAGCGGTGTAAGTGAACGGGTGACATTTTGAAGGTGAATGACCTCT 394
 DB 722 GGGTAAGTCAGAGGTTTAAATGATGAGATGCAATTTTAAATGTTCTGTACTCTTAT 781
 QY 395 ATCAAGATTATATCTTC-----ATTATCTTGAGGATTCCTTAAGATA 439
 DB 782 ACAGGAATCTATTAAGGCTCTGTAGTACGTAATTAAGAAATCTTAATTCGCTCTGCT 841
 QY 440 AATCAATTCCTAAATAAATCTGTGACGTAGTTAAAGCTTCCAGACCGGAAGAGATT 499
 DB 842 AAGAACTCCGACTCGTTTAAATGCCCACTCAGAAATTTGAAGATTTTAAACCGGAG 901
 QY 500 TCATTAATCTTTTACAGGCTCATTTATCAAGACAGAAAGCTGAATTTATTTATGCTTA 559
 DB 902 GGTCTTTAAGGAATGGTGGCTCGTTAGCTAGCAAAATGCCCAATATTTATTTATTCCTT 961
 QY 560 CGTATGTGCAAGCTGCAAAATGTGATTTATTAATTAAGGACGCGATTAAATATATAAA 619
 DB 962 CTTTGTGAGCGCGTGCATTTTTCATTTATTAATACTAAGGATGCTACTAGATATGGA 1021
 QY 620 AAGAAATGGGACTAGTGTGCCACCGTTGATCCAGGGTCAAGGAAATCGATTGTAGC 679
 DB 1022 CTATTTGGGGGCTTAAATGCTACACCTTTTATTA-----ATTATCAAT 1066
 QY 680 AGCGGTTAAAGCGAAATTAAGAGATTAATTAATTTGTAGGGTGTATTAACAAG 739
 DB 1067 CAATACTAGTAGAGCTATTTGAATACTATATCTGATTTTGGTACATTGGTATATAGAG 1126

QY 740 GTTATGATCAGATTAAGACAGCGCGGTACAAAGTCTGAAGTTGGTCCAAATTAATTAAT 799
 DB 1127 GTTTCACGCACTTAAGCAAGAGGCACTGATGCTACAGCTGGTTGAATTTCAATAGAT 1186
 QY 800 TTGATAGAAAGAGCGTGGCGGTATTTGATATTTATTTGATATTTCCAACTATAGATT 859
 DB 1187 ATCGTATAGAGATGACATTTATGATTTATTAATTAAGTACATTTTCAAGTCTTATTA 1246
 QY 860 TTGAAAAATATTCATTTAGCAACAAGTGTAGAGTTAATCAAGGAAATTTATACAGATCCAG 919
 DB 1247 TTACTATATTAACCAATAGAAACAGATTTTTCAGTTGAGTACAGGTCATTTATACGATCCA 1306
 QY 920 TGGGATTTTCAAGGGGAAATTAATGTTGGGAA 951
 DB 1307 TTGGTTTGTATCATCGTAGTAGTCTTAAAGGGA 1338
 RESULT 9
 ID AAV16515 standard; DNA; 3471 BP.
 XX AAV16515;
 AC AAV16515;
 XX 11-JUN-1998 (first entry)
 DT
 XX DNA encoding a *Bacillus thuringiensis* toxin designated 86Bb1(a).
 DE
 XX Toxin; Lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;
 KM *Heliothis virescens*; *Helicoverpa zea*; ss.
 KW *Bacillus thuringiensis*.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3471
 FT /*tag= a
 XX
 FN WO9800546-A2.
 XX
 PD 08-JAN-1998.
 PD
 XX
 PF 01-JUL-1997; 97MO-US011658.
 PR 01-JUL-1996; 96US-00674002.
 PA (MYCO) MYCOGEN CORP.
 PA
 PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhofe BF;
 XX WPI, 1998-086971/08.
 DR P-PSDB; AAW46856.
 XX
 PT New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
 PT encoding toxins which are active against lepidopteran pests such as the
 PT Black cutworm.
 PT
 XX
 PS Example 5; Page 86-89; 183pp; English.
 PS
 XX The present sequence is isolated from a *Bacillus thuringiensis* isolate
 CC (PS86Bb1). It encodes a toxin designated 86Bb1(a) which is active against
 CC lepidopteran pests. The toxin isolates can be used for the control of
 CC lepidopteran pests such as *Agrotis ipsilon* (black cutworm), *Heliothis*
 CC *virescens* and *Helicoverpa zea*. PCR primers and probes can be derived from
 CC the polynucleotide encoding the toxin and used for the amplification and
 CC detection of other toxin-encoding sequences
 CC
 SQ Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
 Query Match 8.5%; Score 172.4; DB 2; Length 3471;
 Best Local Similarity 54.2%; Pred. No. 3.9e-33;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
 QY 161 GGGAAATCAGTCTCGATATATAGTAACTATGGAACATACCTTATCAATTCCTGTAGAAC 220

Db 158 GCGATGCAAGAAAGAGCATATCTATTGGACAACATAGTCTCTTATCAGACAC 217
QY 221 CCGGTATAGTGAATTCCTGTAATATTT-----CAATAATAACCAACTATTCGGT 274
Db 218 CTTCTCTTACTGATTAATTTCAATAGATATAGACCTTAAAGTAAGTAGAGGATA 277
QY 275 CTTCTGGTCAATGTGAGCAGCACTTCTATATGTGATTTAGTATCATTAATTCGTAAG 334
Db 278 GTAGTGGACATCATATCAGATTTGTCTATATGTGACTTATTTATTTATTTGATTTAC 337
QY 335 AGGTAGACAGAGCGGTATTAAGTACGGGGTTGCAATTTTGAAGGTGAATGACTGCTT 394
Db 338 GGGTAGTACAGAGTGTATTAATGATGAGATGAGATTTAAAGTTTCTGACTCTTAT 397
QY 395 ATCAAGATTAATCTCTC-----ATTATCTTGAGATTTGGCTTACAGATA 439
Db 398 ACAGGAATTAATTAAGGCTCTGGAATAGCTGGAATTAAGAACTTAATTCGCTTCGCTG 457
QY 440 AATCAAAATCTTAATAAACTTGCTGACGTAGTTAAAGTTCCAAGCAGCGGAAGAAATT 499
Db 458 AAGAACTCGGTACTCGTTTAAATGCGCAGCTCAGAAATTTGATAGATTTTAAACCCGAG 517
QY 500 TCACTAACTTTTGAAGGCTATTAATCAAGACAGAAAGCTGAATTTATTTATTTGCTTA 559
Db 518 GGTCTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCAAATATTAATTTATTAACCTT 577
QY 560 CGATGTGCAAGCTGCAAAATGTGCATTTATTAATTAAGGGAGCGAGTAAATATAA 619
Db 578 CTTTTCGAGCGCTGCAATTTTCCATTTATTAATTAAGGATGCTACTAGATAGTGGCA 637
QY 620 AAGAAATGGGACTAGTGTGTCCACCGTTATCCAGGGTTCAGGAGAACTGATTTGTAAG 679
Db 638 CTAAATGGGGGCTATCAATAGCTACACCTTTATAA-----ATTATCAAT 682
QY 680 AGCGTTAAAGCGAAATTAAGAGATTAATTAATTTGTTAGGGTGTATTAACAGG 739
Db 683 CAATACTAGTAGCTTATTAAGAACTATATCTATTAATTTGCTGATTAATTCGAG 742
QY 740 GTTATAGTCAAGTAAGCAGCGGGGTACAGTCTGAAGTTTGTGAAATTTAATAAT 799
Db 743 GTTCAACGAACTAAGCAACGAGGCACTAGTCTCAGCTGTGTTAGAAATTTCAATAGAT 802
QY 800 TTCTGAGAGAAATGAGTGGCGGTATTTGATTTATTTGCTATTTTCCAACTTATGATT 859
Db 803 ATGTGAGAGATGACATTTGATTTGATTAATAGATAGATTTTCAAGCTTGATA 862
QY 860 TTGAATAATATTCATTAAGCAACAGGTAGATTTAACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTATTTACCAATTAAGAAACAGATTTTCAGTTGAGTAGGTCATTTATACAGATCAA 922
QY 920 TGGGATATTCAGGGGGAAATTAATGTTGGGA 951
Db 923 TTGGTTTGTACATCGTAGTAGTCTTAAGGGGA 954

RESULT 10
AAK83876
ID AAK83876 standard; DNA; 3471 BP.
XX
AC AAK83876;
XX
DT 09-SEP-1999 (first entry)
XX
DE Bacillus thuringiensis toxin 86Bb1(a) encoding DNA.
XX
KW Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
KM European corn borer; black cutworm; ss.
XX
OS Bacillus thuringiensis.
XX
PN W09933991-A2.
XX
PD 08-JUL-1999.

XX
PF 15-DEC-1998; 98W0-US026585.
XX
PR 31-DEC-1997; 97US-0000285.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Schepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI Muller-Cohn J;
DR WPI; 1999-40513/34.
DR P-PSDB; AAY24959.
XX
PT Method for control of European corn borer using Bacillus thuringiensis
PT toxins.
PS
PS Example 5; Page 90-92; 174pp; English.
XX
CC A method has been developed for the control of European corn borer
CC (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
CC amount of a Bacillus thuringiensis toxin. The method is used for the
CC control of European corn borer (Ostrinia nubilalis). The method can also
CC be used for the control of other non-mammalian pests, particularly black
CC cutworm, and other lepidopteran pests. The present sequence encodes a
CC Bacillus thuringiensis toxin from the present invention
XX
SQ Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
Query Match 8.5%; Score 172.4; DB 2; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3.9e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
QY 161 GGGAAATCGCTCCGATATAGTAATTAATTTGGACATACCTTTACAATTTCTGTAGAAC 220
Db 158 GCGATGCAAGAAAGAGCATATCTATTGGGACAACATAGTCTCTTATCAGACAC 217
QY 221 CCGGTATAGTGAATTCCTGTAATATTTT-----CAATAATAACCAACTATTCGGT 274
Db 218 CTTCTCTTACTGATTAATTTCAATAGATATAGACCTTATAGTAAAGTACTAGAGGATA 277
QY 275 CTTCTGGTCAATCTGTGAGCAGCACTTCTAATGTGATTTAGTATCTATTAATTCGTAAG 334
Db 278 GTAGTGGACAAATCCATATCAGATTTGTCTAATGAGACTTATTAATTAATTTGATTAC 337
QY 335 AGGTAGACAGAGCGGTATTAAGTACGGGGTTCAGATTTTGAAGGTGAATGACTGCTT 394
Db 338 GGTAGTACAGAGTGTTTTAAATGATGAGATTGCAATTTAATGTTCTGTAATCTTAT 397
QY 395 ATCAAGATTAATATCTTC-----ATTATCTGAGATTTGGCTTACAGATA 439
Db 398 ACAGGAATTAATTAAGGCTCTGGAATAGCTGGAATTAAGAACTTAATTTTAAACCCGAG 457
QY 440 AATCAAAATCTTAATAAACTTGCTGACGTAGTTAAAGTTCCAAGCAGCGGAAGAAATT 499
Db 458 AAGAACTCGGTACTCGTTTAAATGCGCAGCTCAGAAATTTGATAGATTTTAAACCCGAG 517
QY 500 TCACTAACTTTTGAAGGCTATTAATCAAGACAGAAAGCTGAATTTATTTATTTGCTTA 559
Db 518 GGTCTTAAACGAATGGTGGCTGTGATTAAGCAAAATGCCAAATATTAATTTATTAACCTT 577
QY 560 CGATGTGCAAGCTGCAAAATGTGCATTTATTAATTAAGGAGCAGGATTAATAATAA 619
Db 578 CTTTTCGAGCGCTGATTTTCCATTTTATTAATTAAGGATGCTACTAGATATAGGATA 637
QY 620 AAGAAATGGGACTAGTGTGTCCACCGTTGATCCAGGGTTCAGGAGAACTGATTTGTAAG 679
Db 638 CTAAATGGGGGCTAATCAATGCTACACCTTTATAA-----ATTATCAAT 682
QY 680 AGCGTTAAAGCGAAATTAAGAGATTAATTAATTTGTTAGGGTGTATTAACAGG 739
Db 683 CAATACTAGTAGCTTATTAAGAACTATATGATTTATTTGCTGATTAATTCGAG 742
QY 740 GTTATAGTCAAGTAAGACAGCGGGGTACAAAGTGTGAAGTTTGTGAAATTTAATAAT 799

Db 743 GTTTCACGACCTTAAGACACAGAGCATTAGTGGTCTTGGTGAATTTCAATAT 802
Qy 800 TTGCTAGGAATGACGTTGGCGGATTTGATATATTTCTATATTTCTTATGAT 859
Db 803 ATCGTAGAGAGATGACATTTGATATATATGATGATATTTTCAAGTCTGATA 862
Qy 860 TTGAAAAATATCTTACGACCAAGGTAGAGTTTACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTAATTTACCCATATGAAAACAGATTTTCAGTTGAGAGGTCATTTATACAGATCCAA 922
Qy 920 TGGATATTTGAGGGGAAATTTATGTTGGGAA 951
Db 923 TTGGTTTGTATCATCGTAGTAGTCTTAGGGGA 954

RESULT 11
AAS02478
ID AAS02478 standard; DNA; 2407 BP.
AC AAS02478;
AT 29-AUG-2001 (first entry)
XX B. thuringiensis DNA encoding a toxic crystal protein, CryET60.
XX
XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
XX transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
XX sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
XX pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
XX cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
XX cotton leaf perforator; CryET60; ds.
XX
XX Bacillus thuringiensis.
XX OS
XX
XX Key Location/Qualifiers
XX FT 1..2406
XX FT /*tag= a
XX FT /product= "CryET60"
XX FT /partial
XX FT /note= "No stop codon"
XX PN W0200119859-A2.
XX PD 22-MAR-2001.
XX PF 13-SEP-2000; 2000WO-US025361.
XX PR 15-SEP-1999; 99US-0153995P.
XX PA (MONS) MONSANTO CO.
XX PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX DR WPI; 2001-281518/29.
XX DR P-PSDB; AAU02035.
XX PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
XX PT and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 17; Page 127-128; 173pp; English.

The sequence encodes a B. thuringiensis lepidopteran-active delta-endotoxin, crystal protein CryET60. The lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polynucleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,

CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification)
XX
SQ Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;
Query Match 8.1%; Score 162.8; DB 4; Length 2407;
Best Local Similarity 53.4%; Pred. No. 9.4e-31;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;
Qy 161 GGGATATGCTCGGATATAGTACTATTTGGGACATACCTTATCAATTTCTGTAGAAC 220
Db 158 GCGATGACGAAAAAGACGATATCTATTTGGGACACATAGTCTCTTATACAGACAC 217
Qy 221 CCGGTATAGGTGGAATTCCTGTATATATTTT-----CAATTAATAACAACTACATCCGT 274
Db 218 CTCTCTTACTGAGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACTAGAGGTA 277
Qy 275 CTCTGTGCAATCTGTGGACACACTTTCTATATGTATATATATATATATTTGTAAG 334
Db 278 GTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATATATATATATATAT 337
Qy 335 AGTAGACGAGAGGTGTATAGTACGAGGGTTGCAATTTGAGGGTGAATGACTGCTT 394
Db 338 GGGTATGTCAGAGGTTTAAATGATGAGATTTGAATTTAAATGTTGTTGTTGTTACTTAT 397
Qy 395 ATCAAGATTTATATCTTC-----ATTATCTGAGAGTTGGCTTACAGATA 439
Db 398 ACAGAACTTTATAGAGCTCTGTATAGCTGGAATTAAGATCTTAATTTCTGCTGTG 457
Qy 440 AATCAATCTTAAAAAACTTGCTGACCTAGTTAAACAGTTTCAACACAGGAGAAAGATT 499
Db 458 AAGAACTCCGTAACCTGTTTAAATGATGCGCAGCTCAGATTTGATAGATTTTAAACCGAG 517
Qy 500 TCACTAACTTTTACAGAGGCTCATTTACAAAGACAAAGCTGAATATTTATTTGCTTA 559
Db 518 GGTCTTTTAAAGAAATGAGTGGCTGTTAGCTAGACAAATATGCCCCAAATTTATTTACTT 577
Qy 560 CGTATGCAAGCTGCAATATGTCATTTATTAATTAAGGAGGAGCTTAATATATAA 619
Db 578 CTTTTCGAGCGCTGCAATTTTTCATTTTATTACTTAAGGAGTCTACTAGATATGGA 637
Qy 620 AAGAAATGGGAGCTAGTGTGTCAACCGTTGATCCAGGGTCAAGGAACTGATTTGTAACG 679
Db 638 CTAAATGGGGCTATTAACAATGTACACCTTTTATA-----ATTATCAAT 682
Qy 680 AGCGTTTAAAGCAAAATTAAGATTAATTTTGTGTAGGGTGTATTAACAAG 739
Db 683 CAAAACCTAGTAGAGCTTATGAACTATATATCTGATTTATGCTATGATTTGGGATATCGAG 742
Qy 740 GTTTAGATCAGATTAAGACAGCGGGTACAGTGTCTGAAGTTTGGTGAATTTTATATAAT 799
Db 743 GTTCAACCGAATTAAGACAGAGGCTTATGCTTACAGCTTGTATGAATTTATATGAT 802
Qy 800 TTGCTAGGAATGACCTTGGCGGATTTGATATATTTGCTATATTTTCAACTTATGAT 859
Db 803 ATCGTAGAGAGATGACATTTGATATATATGATGATTAATAATAGATCATTTTCAAGTCTGATA 862
Qy 860 TTGAAAAATATCTTACGACCAAGGTAGAGTTTACTAGGAAATTTATACAGATCCAG 919
Db 863 TTACTAATTTACCCATATGAAAACAGATTTTCAGTTGAGAGGTCATTTATACAGATCCAA 922
Qy 920 TGGATATTTGAGGGGAAATTTATGTTGGGAA 951
Db 923 TTGGTTTGTATCATCGTAGTAGTCTTAGGGGA 954

RESULT 12
AEA61394
ID AEA61394 standard; DNA; 4391 BP.
AC AEA61394;

QY 1902 TGACATCCAAATGTAAGAAATGTCATTCAGAGACATATGTAGATGCA 1961
 DB 2638 TAAATATGAAATTCCTCCCACTACGTATACCATTCACA-----GGAAATATGCA 2686
 QY 1962 AGAGTCAATCTCTGGAAACAAAAGAGATTGTAATGTTATTTATCAATTTAA 2019
 DB 2687 GGAATAATATGAAATTAAGAAATGTCACAGAAACATTTATATGTTATTTGATTTAA 2744

RESULT 13
 AAS02466
 ID AAS02466 standard; DNA; 1959 BP.
 XX AAS02466;
 AC AAS02466;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE B. thuringiensis DNA encoding a toxic crystal protein, CryET43.
 XX
 KM Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 KM transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
 KM sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 KM pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 KM cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 KM cotton leaf perforator; CryET43; ds.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT 1..1959
 FT /*tag= a
 FT /product= "CryET43"
 FT /partial
 FT /note= "No stop or start codon"
 XX
 PN MO200119859-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US025361.
 XX
 PR 15-SEP-1999; 99US-0153995P.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 DR WPI: 2001-281518/29.
 DR P-PSDB; AAU02023.
 XX
 PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 PT insect resistance of plant.
 XX
 PS Claim 17; Page 105; 173pp; English.
 XX
 CC The sequence encodes a B. thuringiensis Lepidopteran-active delta-
 CC endotoxin, crystal protein CryET43. The Lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification)
 CC
 XX
 SO Sequence 1959 BP; 646 A; 348 C; 393 G; 572 T; 0 U; 0 Other;

Query Match 5.9%; Score 119.8; DB 4; Length 1959;
 Best Local Similarity 55.0%; Pred. No. 7.6e-20;
 Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

QY 435 AGATTAATCAAACTCTGTAAGAAATGTCATTCAGAGACATATGTAGATGCA 494
 DB 411 AGATTAATCAAACTCTGTAAGAAATGTCATTCAGAGACATATGTAGATGCA 470
 QY 495 AGATTTCACTAACTTTTACAGAGGCTCATTTATCAAGAGAAAGCTGAAATATTTATTT 554
 DB 471 ACTTGACATTAACATCTCTATACCGCTTTTCAGAAATGCAAAATGAAAGCTCATTTATTT 530
 QY 555 GCTTACGTATGTCAGAGCTGCAAAATGTCATTTATTAATTAAGAGGACGCTTAAATA 614
 DB 531 AATGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGCCATCCCTTTT 590
 QY 615 TAAAAAAGATGGGAGCTAGTGTCTCCACCGTTGTATCCAGGGTCAGAGAACTGATTTG 674
 DB 591 TGGTAGTAATGGGGATGGCATCTTCCATGTTAACCA-----TA 632
 QY 675 TAAAGAGCGGTTAAAGCGAAATTAAGAGATTAATTTATTTGTTAGGGTGTATTTAA 734
 DB 633 TTACAGAGAACAAAATGCAATATACAGAGAAATTTCTTACCATTTGCTTACAAATGTTATTA 692
 QY 735 CAAGGCTTTAGATCAGATTAAGACAGAGCGGTACAAAGTCTGAAGTTTGTGCAAAATTTAA 794
 DB 693 TACAGGGCTTAATTAATTAAGA-----GGACAAATGCTGAAGTTTGTGCGGTATTTAA 746
 QY 795 TAAATTTCTGTAAGAAATGACGTTGGCGGTATTTGATTTATTTGCTATATTTCCACTTA 854
 DB 747 TCAATTCCTGTAAGACCTTAACGTTAGGGGTATTTAGATTTGTGTCCTTATTTCCACACTA 806
 QY 855 TGAATTTGAAATTAATCATTTAGCAACAAGTGTAGAGTAACTTAAAGGAAATTTTAAACA 914
 DB 807 TGATTAATCGCATTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 866
 QY 915 TCCAGTGGATTAATTCAGAGGGAATTAATGTTGGGAACGTTTGTGCTTTTAAAT 969
 DB 867 TCCAAATGGAGAAACAAATGCACTTCAGATTTTGGCAATGCAATGTTGTTTAAAT 921

RESULT 14
 ADR89411
 ID ADR89411 standard; cDNA; 1986 BP.
 XX
 AC ADR89411;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE AXMI-009 alternative start site coding sequence #2.
 XX
 KM 86; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KM expression cassette; transformation; transgenic plant; bacteria;
 KM lepidoptera; coleoptera; pest; pesticide; resistance;
 KM pesticidal activity.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT 1..1986
 FT /*tag= a
 FT /product= "Alternative AXMI-009 #2"
 XX
 PN WO2004074462-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005829.
 XX
 PR 20-FEB-2003; 2003US-0448632P.
 PR 20-FEB-2003; 2003US-0448633P.
 PR 20-FEB-2003; 2003US-0448797P.

PR 20-FEB-2003; 2003US-0448806P.
 PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 (ATHE-) ATHENIX CORP.
 PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
 XX MPI: 2004-635574/61.
 DR P-PSDB; ADR89412.
 XX
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 PS Claim 1; SEQ ID NO 23; 178bp; English.
 XX
 CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX
 XX Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other:
 Query Match 5.9%; Score 118.4; DB 13; Length 1986;
 Best Local Similarity 51.3%; Pred. No. 1,7e-19;
 Matches 544; Conservative 0; Mismatches 426; Indels 90; Gaps 8;

Db 916 ACTTACCCCTGGTATATTCCTATATATACAACTTTACGCTATATGAAATATACGGAAGA 975
 Qy 991 CGGGACCTGGTTTACCTTACCTTCAAGCTATATATATATATATATATATATATATATAT 1050
 Db 976 CGACGCTCTTCTTATATACCACTTGGCTTATCTTATATTTTATATATATATATATATATAT 1035
 Qy 1051 CTTCAGCTTGTATCTTAT 1110
 Db 1036 AATATGCTGATGTGAGAAATATTTGGGAGGCATACATTAGTTGAAATGGAATATGAT 1095
 Qy 1111 GGTACGCGTCTTTTCAAGCTATGTCTGACATACAGATATATATATATATATATATATAT 1167
 Db 1096 GGTCTGAAAT 1155
 Qy 1168 ATTTTGTGCAAT 1221
 Db 1156 AATTTGCGCAACCTTCTCTGTTTCAATATATATATATATATATATATATATATATAT 1215
 Qy 1222 CAACGTTTGTGGGATTCATATCCAGGCAATCTTGTTCAGTGCAGATATATATATATAT 1281
 Db 1216 ACHAGAGCTAAT 1275
 Qy 1282 ACAACACTAATA-----CTTCTGTATGAGTAAACAGTTCTGGTACTCA 1329
 Db 1276 TCAAT 1335
 Qy 1330 CAGACATATGATCTGTGTAT 1389
 Db 1336 CAACAT 1392
 Qy 1390 TACTCAT 1431
 Db 1393 TTACGCAAT 1452
 Qy 1432 ACTTCAGAGTTAAGTAT 1491
 Db 1453 ATTTGATGCTTTTAAAGTTTGTGGGCACTACCAAGTATGATGATATATATATATATAT 1512
 Qy 1492 TATCCAGAT 1531
 Db 1513 GAACCAAT 1552
 RESULT 15
 ADR89409
 ID ADR89409 standard; cDNA; 2016 BP.
 AC ADR89409;
 XX
 AC ADR89409;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE AXMI-009 alternative start site coding sequence.
 XX
 DE ss: gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX
 OS Bacillus thuringiensis.
 XX
 OS
 XX
 FT Key Location/Qualifiers
 FT CDS 1..2016
 FT /tag= a
 FT /product= "Alternative AXMI-009"
 PD MO2004074462-AA.
 XX
 PD 02-SEP-2004.
 XX
 XX 20-FEB-2004; 2004WO-US005829.
 PF 20-FEB-2004; 2004WO-US005829.
 XX
 XX 20-FEB-2003; 2003US-0448632P.
 PR

Page Blank (uspo)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:29:27; Search time 1098.23 Seconds

(without alignments)
15202.512 Million cell updates/sec

Title: US-10-782-141-2

Perfect score: 2019
1 gtgaaaaaatgaattctta.....atagttattatcaattaa 2019

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA_Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	2019	8	US-10-782-141-2
2	2019	100.0	2145	8	US-10-782-141-1
3	2010	99.6	2010	8	US-10-782-141-4
4	747.2	37.0	2082	8	US-10-781-979-2
5	747.2	37.0	5980	8	US-10-781-979-1
6	739.8	36.6	2073	8	US-10-781-979-4
7	172.4	8.1	3471	5	US-10-099-285-71
8	162.8	8.1	2407	6	US-10-428-961-29
9	133.6	6.6	4391	9	US-10-929-754-4
10	119.8	5.9	1959	6	US-10-428-961-5
11	117.6	5.8	1806	8	US-10-782-020-4
12	117.6	5.8	1890	8	US-10-782-020-2
13	116.8	5.8	2190	8	US-10-782-020-1
14	116.8	5.8	3684	6	US-10-428-961-62
15	113.4	5.6	2019	7	US-10-665-460A-7
16	112.4	5.6	3687	7	US-10-665-460A-1
17	112.4	5.6	4173	6	US-10-428-961-37
18	111.8	5.5	2019	7	US-10-665-460A-3
19	111.8	5.5	2019	7	US-10-665-460A-1
20	111.8	5.5	3471	5	US-10-099-285-73
21	111.8	5.5	3471	5	US-10-428-961-27
22	111.8	5.5	4344	9	US-10-687-879A-4
23	110.8	5.5	1561	9	US-10-687-879A-2

24	110.2	5.5	2019	7	US-10-665-460A-5	Sequence 5, Appl1
25	105.4	5.2	2019	7	US-10-665-460A-11	Sequence 11, Appl1
26	105	5.2	1860	5	US-10-032-717-19	Sequence 19, Appl1
27	105	5.2	1860	6	US-10-414-637-19	Sequence 19, Appl1
28	105	5.2	1860	7	US-10-606-320-15	Sequence 15, Appl1
29	105	5.2	1860	8	US-10-746-914-15	Sequence 15, Appl1
30	105	5.2	2003	5	US-10-032-717-5	Sequence 5, Appl1
31	105	5.2	2003	6	US-10-414-637-5	Sequence 5, Appl1
32	105	5.2	2010	5	US-10-032-717-15	Sequence 15, Appl1
33	105	5.2	2010	6	US-10-414-637-15	Sequence 15, Appl1
34	105	5.2	2010	7	US-10-606-320-11	Sequence 11, Appl1
35	105	5.2	2010	8	US-10-746-914-11	Sequence 11, Appl1
36	105	5.2	3621	5	US-10-032-717-1	Sequence 1, Appl1
37	105	5.2	3621	6	US-10-414-637-1	Sequence 1, Appl1
38	105	5.2	3621	7	US-10-606-320-1	Sequence 1, Appl1
39	105	5.2	3621	8	US-10-746-914-1	Sequence 1, Appl1
40	105	5.2	3621	10	US-11-021-115-5	Sequence 5, Appl1
41	105	5.2	4874	5	US-10-032-717-27	Sequence 27, Appl1
42	105	5.2	4874	6	US-10-414-637-27	Sequence 27, Appl1
43	105	5.2	4874	7	US-10-606-320-17	Sequence 17, Appl1
44	105	5.2	4874	8	US-10-746-914-17	Sequence 17, Appl1
45	104.4	5.2	3687	8	US-10-809-953-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-10-782-141-2
Sequence 2, Application US/10782141
Publication No. US20040197917A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargis, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Cart, Brian
TITLE OF INVENTION: AXMT-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for its Use
FILE REFERENCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,632
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2019
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-10-782-141-2
Query Match 100.0%; Score 2019; DB 8; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAAATATGATTTCTTATCAAAATATCAAAATATGAAATTTGATGTTCCCG 60
Db 1 GTGAAATATGATTTCTTATCAAAATATCAAAATATGAAATTTGATGTTCCCG 60
QY 61 AATTAACAATATGCAATGCAAGATATCTTTGCAAGATCAATATATTTCCAT 120
Db 61 AATTAACAATATGCAATGCAAGATATCTTTGCAAGATCAATATATTTCCAT 120
QY 121 AACCTGACGCTTGTGACGAGGACGATGCAAGATACGTGGATCAGTCTCGATATA 180
Db 121 AACCTGACGCTTGTGACGAGGACGATGCAAGATACGTGGATCAGTCTCGATATA 180
QY 181 GTAACTATTGGACATACCTTATACAAATTTCTGTAACCCGCTATAGTGAATTCCT 240
Db 181 GTAACTATTGGACATACCTTATACAAATTTCTGTAACCCGCTATAGTGAATTCCT 240

Db 181 GTAATATGCGGACATACCTTATACAAATCTGCTAGAACCCGGTATAGAGTAATCCCT 240
QY 241 GTAATATTTTCATTAATAAACAACATCATCGCTCTTCTGCTAACTGAGGAGACCT 300
Db 241 GTATATTTTTCATTAATAAACAACATCATCGCTCTTCTGCTAACTGAGGAGACCT 300
QY 301 TCTATATGATTTAGATCTATTAATTCGTAAGAGGTAGACGAGCGGTAAAGTAC 360
Db 301 TCTATATGATTTAGATCTATTAATTCGTAAGAGGTAGACGAGCGGTAAAGTAC 360
QY 361 GGGGTTCAGATTTTGAAGGTGAATGACCTGCTTATCAGATTATTAATCTTACTT 420
Db 361 GGGGTTCAGATTTTGAAGGTGAATGACCTGCTTATCAGATTATTAATCTTACTT 420
QY 421 GAGATTTGCTTACAGTAAATCAAAATCTTAAATCTGCTACGAGTAAACGTTCC 480
Db 421 GAGATTTGCTTACAGTAAATCAAAATCTTAAATCTGCTACGAGTAAACGTTCC 480
QY 481 CAAGCAGGGAGAGAATTTCACTAACTTTTACAGGGGTCAATTAACAAGACAGAAAGCT 540
Db 481 CAAGCAGGGAGAGAATTTCACTAACTTTTACAGGGGTCAATTAACAAGACAGAAAGCT 540
QY 541 GAAATATATTTATTTGCTACGTATGTCGAAGCTGCAAAATGTCATTTATTAATTAAG 600
Db 541 GAAATATATTTATTTGCTACGTATGTCGAAGCTGCAAAATGTCATTTATTAATTAAG 600
QY 601 GACGAGTTAATATATAAAGATGGGACCTAGTGTGTCACCGTTGATCCAGGGTCA 660
Db 601 GACGAGTTAATATATAAAGATGGGACCTAGTGTGTCACCGTTGATCCAGGGTCA 660
QY 661 GGGAGAACTGATTTGTAAACGAGCGGTTAAAGCGAAATAAAGAGTAACTAAATTAATG 720
Db 661 GGGAGAACTGATTTGTAAACGAGCGGTTAAAGCGAAATAAAGAGTAACTAAATTAATG 720
QY 721 GTAGGTTGATTAACAAGGTTTATGATCAATAAGACAGCGGGTACAGTGTCTGAAGT 780
Db 721 GTAGGTTGATTAACAAGGTTTATGATCAATAAGACAGCGGGTACAGTGTCTGAAGT 780
QY 781 TGGTCAAAATTTTATTAATTTCTGTAAGAAATGACGTTGGCGGTAATTAATTAATGCT 840
Db 781 TGGTCAAAATTTTATTAATTTCTGTAAGAAATGACGTTGGCGGTAATTAATTAATGCT 840
QY 841 ATATTTCCAACTTATGATTTTGAATAATATCAATTCGTAAGCAAGTGTAGATTAAGTAC 900
Db 841 ATATTTCCAACTTATGATTTTGAATAATATCAATTCGTAAGCAAGTGTAGATTAAGTAC 900
QY 901 GAAATTTATACATTCAGTGGGATTTTCAGGGGAAATTAATGCTTGGGAAACGTTTCTT 960
Db 901 GAAATTTATACATTCAGTGGGATTTTCAGGGGAAATTAATGCTTGGGAAACGTTTCTT 960
QY 961 AGCTTAAATTCGGTAAAGCAAAATGGAACAGGGGACCTGCTTATGTTACTTGGCTTCAA 1020
Db 961 AGCTTAAATTCGGTAAAGCAAAATGGAACAGGGGACCTGCTTATGTTACTTGGCTTCAA 1020
QY 1021 GCTATAGATTAATATGATCTTATTAATCTTCACTGCTGCTTATCTTAAGTGGCTGAG 1080
Db 1021 GCTATAGATTAATATGATCTTATTAATCTTCACTGCTGCTTATCTTAAGTGGCTGAG 1080
QY 1081 GGAACCTGCTATTAATGACCTTCACAAAGGGTAAACGCTGCTTCAACGATGCTCGGA 1140
Db 1081 GGAACCTGCTATTAATGACCTTCACAAAGGGTAAACGCTGCTTCAACGATGCTCGGA 1140
QY 1141 ACTAGAGTAAATATCAAGTAAATTAATTTTGGCAATTCGATTAATTAATTAATTAAT 1200
Db 1141 ACTAGAGTAAATATCAAGTAAATTAATTTTGGCAATTCGATTAATTAATTAATTAAT 1200
QY 1201 TCAATAGTATGATGATGCAATGCAACCGTTTGGTATTCATTCACGAGCATCTTGT 1260
Db 1201 TCAATAGTATGATGATGCAATGCAACCGTTTGGTATTCATTCACGAGCATCTTGT 1260
QY 1261 TCACTGTCAGAAATTTTTCGACAACTAAATCTTCTGATAGAGGTAACAGTTCT 1320
Db 1261 TCACTGTCAGAAATTTTTCGACAACTAAATCTTCTGATAGAGGTAACAGTTCT 1320

QY 1321 GGGTACTCAGACAAATGGAATCTGNGTTACAGGATTAATTAAGATCTACACCTACT 1380
Db 1321 GGGTACTCAGACAAATGGAATCTGNGTTACAGGATTAATTAAGATCTACACCTACT 1380
QY 1381 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGGATGTTCAAAATGAACCTTCAGA 1440
Db 1381 CGTACAAATTTACTCTCATAGATTTATCAAAATGCGGATGTTCAAAATGAACCTTCAGA 1440
QY 1441 GTTAACGATTTTGGTTGACACATACAGTATGAATAAAGATTAATCGAATTTATCCAGAT 1500
Db 1441 GTTAACGATTTTGGTTGACACATACAGTATGAATAAAGATTAATCGAATTTATCCAGAT 1500
QY 1501 AAAATTAAGCAATTTCTGACATTAAGGTTTGGCTTACAGGAGGTACAGGATATGCA 1560
Db 1501 AAAATTAAGCAATTTCTGACATTAAGGTTTGGCTTACAGGAGGTACAGGATATGCA 1560
QY 1561 GGAAGTTACGTACAGCTGGGCTGGTTATACAGAGAGAGATGTAGTAACTTACCTTAT 1620
Db 1561 GGAAGTTACGTACAGCTGGGCTGGTTATACAGAGAGAGATGTAGTAACTTACCTTAT 1620
QY 1621 CAAGCAAGTTTAAATATAGTTTAACTTGTGACCCAGATTAATAATTAACGTTTGA 1680
Db 1621 CAAGCAAGTTTAAATATAGTTTAACTTGTGACCCAGATTAATAATTAACGTTTGA 1680
QY 1681 CTTGCTACGAGAGTGGAGACCTGGTCCGTTCCGAGTGAAGAAATGGTCCGCAAGTTCT 1740
Db 1681 CTTGCTACGAGAGTGGAGACCTGGTCCGTTCCGAGTGAAGAAATGGTCCGCAAGTTCT 1740
QY 1741 GTTCAATATGCTAATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTGATTAATG 1800
Db 1741 GTTCAATATGCTAATTTTCTGTCAGCTACAGGTGCTATAGTTCAATTTGATTAATG 1800
QY 1801 GACACCTTATGTTACTTATTAATCAATACAGGTGTTGAATAATTAATCAAAATCTATCT 1860
Db 1801 GACACCTTATGTTACTTATTAATCAATACAGGTGTTGAATAATTAATCAAAATCTATCT 1860
QY 1861 GGTACCACTTATTTGTTGACAAAGTCGAATTTATCCCAATGACATCCAAATTTGAAAA 1920
Db 1861 GGTACCACTTATTTGTTGACAAAGTCGAATTTATCCCAATGACATCCAAATTTGAAAA 1920
QY 1921 TGTACGAATGTCAATTCGAAGAGACATATGTAGATGTGAAGAGTCAATCTTGGAA 1980
Db 1921 TGTACGAATGTCAATTCGAAGAGACATATGTAGATGTGAAGAGTCAATCTTGGAA 1980
QY 1981 ACMAAAGAGATTTGTAATGTTTATTTATCAATTAA 2019
Db 1981 ACMAAAGAGATTTGTAATGTTTATTTATCAATTAA 2019

RESULT 2
US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Kozel, Michael G.
; APPLICANT: Duck, Michael B.
; TITLE OF INVENTION: AKM1-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis

US-10-782-141-1

Query Match	100.0%;	Score 2019;	DB 8;	Length 2145;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2019; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	TTGAAAAATAGAAATCTTATCAAAATCAANTGAATGAATGAATTCGGATGGTCCCG	60
Db	127	GTGAAAATATGAATTTCTTATCAAAATCAANTGAATGAATGAATTCGGATGGTCCCG	186
QY	61	AATAACACAAATATGTCCAAACAGATATCTTTTGCAAGAGATCCAAATATATTTCTATT	120
Db	187	AATAACAAATATGTCCAAACAGATATCTTTTGCAAGAGATCCAAATATATTTCTATT	246
QY	121	AACCTGACGTTGTCCAGGGAAGGCCATGCGCAAGATACGTGGGAATCAGTCTCGGATATA	180
Db	247	AACCTGACGTTGTCCAGGGAAGGCCATGCGCAAGATACGTGGGAATCAGTCTCGGATATA	306
QY	181	GTAACTATTTGGGACATACCTATATCAATTTCTTGCAAGAACCCGGATATGGGGAATTCCT	240
Db	307	GTAACTATTTGGGACATACCTATATCAATTTCTTGCAAGAACCCGGATATGGGGAATTCCT	366
QY	241	GTAAATATTTTCAATATATTAACAACTCAATCCGCTTCGTGTCATCTGTGGGACACTT	300
Db	367	GTAAATATTTTCAATATATTAACAACTCAATCCGCTTCGTGTCATCTGTGGGACACTT	426
QY	301	TCTATATGTGATTTAGTATCTATATATTTGTTAAAGAGTGAACGAGCGTGTAAGTGAC	360
Db	427	TCTATATGTGATTTAGTATCTATATATTTGTTAAAGAGTGAACGAGCGTGTAAGTGAC	486
QY	361	GGGGTTGCAGATTTTGGAGGGTGAATGACGTGCTATCAAGATTTATCTTCAATTATCTT	420
Db	487	GGGGTTGCAGATTTTGGAGGGTGAATGACGTGCTATCAAGATTTATCTTCAATTATCTT	546
QY	421	GAGGATTTGCGCTTACAGATTAATCAATCTCTAAAAAACTTGTCTGACGTATGTTAAACAGTTC	480
Db	547	GAGGATTTGCGCTTACAGATTAATCAATCTCTAAAAAACTTGTCTGACGTATGTTAAACAGTTC	606
QY	481	CAAGCAGAGGGAAGAAGATTTCACCTTAACTTTTACAGAGGTCAATTATCAAGACAGAAGCT	540
Db	607	CAAGCAGAGGGAAGAAGATTTCACCTTAACTTTTACAGAGGTCAATTATCAAGACAGAAGCT	666
QY	541	GAATATTTATTAATTTGCGCTTACGTATGTGCAAGCTCAAAATGTGCATTTATCTATTAAGG	600
Db	667	GAATATTTATTAATTTGCGCTTACGTATGTGCAAGCTCAAAATGTGCATTTATCTATTAAGG	726
QY	601	GACGCAGTTAAATATTAATAAATAAAGAAATGGGGAATGAGTGTGTCCACCGTGTATCCAGGCTCA	660
Db	727	GACGCAGTTAAATATTAATAAATAAAGAAATGAGTGTGTGTCCACCGTGTATCCAGGCTCA	786
QY	661	GGGGAACCTGATTTGTTAATCGAGCGGTTTAAACGCAAAATTAANAAGATATCTAATTAATGT	720
Db	787	GGGGAACCTGATTTGTTAATCGAGCGGTTTAAACGCAAAATTAANAAGATATCTAATTAATGT	846
QY	721	GTAGGCTGTATTAACAAGGCTTTTATGATTCAGATTAAGACAGCGGGTATCAAGTCTGAAGTT	780
Db	847	GTAGGCTGTGTATTAACAAGGCTTTTATGATTCAGATTAAGACAGCGGGTATCAAGTCTGAAGTT	906
QY	781	TGCTGCAAAATTTAATAAATTTCTGTAGAGAAATGACGTTCGGCGGTATTTGATTAATTTGCT	840
Db	907	TGCTGCAAAATTTAATAAATTTCTGTAGAGAAATGACGTTCGGCGGTATTTGATTAATTTGCT	966
QY	841	ATATTTTCAACTTATATGATTTTGAAGAAATATCCATTAGCAACAATGTAGATTAACATGAG	900
Db	967	ATATTTTCAACTTATATGATTTTGAAGAAATATCCATTAGCAACAATGTAGATTAACATGAG	1026
QY	901	GAATTTTATACAGATTCAGATGAGGATTTTCAAGGGGAAATTAATGTGTGGGAACGATTTT	960
Db	1027	GAATTTTATACAGATTCAGATGAGGATTTTCAAGGGGAAATTAATGTGTGGGAACGATTTT	1086
QY	961	AGCTTTAATTCGGTATGAAGCAAAATGGAACAACGGGGAACCTGGTATTAATGTTACTTGGCTTCAA	1020
Db	1087	AGCTTTAATTCGGTATGAAGCAAAATGGAACAACGGGGAACCTGGTATTAATGTTACTTGGCTTCAA	1146

Qy	1021	GCATACGATATATATATGACATTCATTTAAATCTTGACGCTGGTATCTTTAGGCGTGGGGG	1080
Db	1147	GCTATAGATATATATATGACATTCATTTAAATCTTGACGCTGGTATCTTTAGGCGTGGGGG	1206
Qy	1081	GGAACCTGCTATATATATGAAAGCTTCCAAAGGGTAAACGGTGGCTTTTCAACGATGCTTGA	1140
Db	1207	GGAACCTGCTATATATATGAAAGCTTCCAAAGGGTAAACGGTGGCTTTTCAACGATGCTTGA	1266
Qy	1141	ACTACGAGTATATATCCACGTAATATATTTTGGCAATACCGATATATTTAAATTAAT	1200
Db	1267	ACTACGAGTATATATCCACGTAATATATTTTGGCAATACCGATATATTTAAATTAAT	1326
Qy	1201	TCATTAGCTGATATGCAATGCAACGGTTTGGGGATTTCAATCCACGGCATCTGTT	1260
Db	1327	TCATTAGCTGATATGCAATGCAACGGTTTGGGGATTTCAATCCACGGCATCTGTT	1386
Qy	1261	TCACGTGACAGATTTTTCGCAACAACATAATCTTTCCTGATATGAGGTAAACAGTCT	1320
Db	1387	TCACGTGACAGATTTTTCGCAACAACATAATCTTTCCTGATATGAGGTAAACAGTCT	1446
Qy	1321	GGGTACTCACAGACAAATTGATCTGTGTACACGATATTAATTAAGATCTACACCTAGT	1380
Db	1447	GGGTACTCACAGACAAATTGATCTGTGTACACGATATTAATTAAGATCTACACCTAGT	1506
Qy	1381	CGTACAAATTAATCTCTACATATTAATCAAAAGCGGCATGCTTCAAAATGAAACCTCCAGA	1440
Db	1507	CGTACAAATTAATCTCTACATATTAATCAAAAGCGGCATGCTTCAAAATGAAACCTCCAGA	1566
Qy	1441	GTTAACGTATTTGGTTGGACACATACAGATATGAAAAAGATATCCAAATTTATCCAGAT	1500
Db	1567	GTTAACGTATTTGGTTGGACACATACAGATATGAAAAAGATATCCAAATTTATCCAGAT	1626
Qy	1501	AAAATTAACGAAATTCCTCGACATTAAGCTTTTGCCCTACACAGCATGACAGATATGCA	1560
Db	1627	AAAATTAACGAAATTCCTCGACATTAAGCTTTTGCCCTACACAGCATGACAGATATGCA	1686
Qy	1561	GGAGGTAAACGTACAGCTGGGGCCGTGTTATACAGAGAGAGATGATGATAGGTTACCTTAT	1620
Db	1687	GGAGGTAAACGTACAGCTGGGGCCGTGTTATACAGAGAGAGATGATGATAGGTTACCTTAT	1746
Qy	1621	CAAGCAAGTTTAAATAATACGTTTAACTTCTGCAACCCACGAATAAATAATCCGTTGAGA	1680
Db	1747	CAAGCAAGTTTAAATAATACGTTTAACTTCTGCAACCCACGAATAAATAATCCGTTGAGA	1806
Qy	1681	CTTGCGTACCGGAGTGGAGACCTGGTCCGTTCCGATAGAAAAGATGCTGCCAGATTCT	1740
Db	1807	CTTGCGTACCGGAGTGGAGACCTGGTCCGTTCCGATAGAAAAGATGCTGCCAGATTCT	1866
Qy	1741	GTTTCAAAATGCTAATTTTTCTCGTCCAGCTACACAGGGGCTATATGTTCAATTTGATATGNG	1800
Db	1867	GTTTCAAAATGCTAATTTTTCTCGTCCAGCTACACAGGGGCTATATGTTCAATTTGATATGNG	1926
Qy	1801	GACACCTTAGTACTACATTTAATCAATCAATCAGTGTGTAATTAATTAACAAATCTATCT	1860
Db	1927	GACACCTTAGTACTACATTTAATCAATCAATCAGTGTGTAATTAATTAACAAATCTATCT	1986
Qy	1861	GGTTACCACTTATTTGTTGCAAAAGTCGAATTTATCCCAATTGACATCCAAATTTGAAAA	1920
Db	1987	GGTTACCACTTATTTGTTGCAAAAGTCGAATTTATCCCAATTGACATCCAAATTTGAAAA	2046
Qy	1921	TGTACGAAATGTCAATTCGAAAGGACATATGATGATGTAAGAGATGCAAAATCCTTGAA	1980
Db	2047	TGTACGAAATGTCAATTCGAAAGGACATATGATGATGTAAGAGATGCAAAATCCTTGAA	2106
Qy	1981	ACAAAAAAGAGATGTGTAATTAATTTATCAATTTAA 2019	
Db	2107	ACAAAAAAGAGATGTGTAATTAATTTATCAATTTAA 2145	

```
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carotzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ. ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
US-10-782-141-4
```

```
Query Match          99.6%; Score 2010; DB 8; Length 2010;
Best Match Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 ATGAATCTTATCAAAATACAAATGAATATGAATTCGTGATGGTCCCGAATTAACACA 69
DB 1 ATGAATCTTATCAAAATACAAATGAATATGAATTCGTGATGGTCCCGAATTAACACA 60
QY 70 AATATGCAACAGATATCTTTTGCAAGATCCAAATATTTTCTATTAACCTGGAC 129
DB 61 AATATGCAACAGATATCTTTTGCAAGATCCAAATATTTTCTATTAACCTGGAC 120
QY 130 GCTTGTCAGGGAAGGCCATGGAAGATACGTGGGAATCAGTCCGATATAGTACATT 189
DB 121 GCTTGTCAGGGAAGGCCATGGAAGATACGTGGGAATCAGTCCGATATAGTACATT 180
QY 190 GGAACATACCTTATACAAATCTTGCTAGAACCCGGTATAGTGGAAATTCCTGTATATTT 249
DB 181 GGAACATACCTTATACAAATCTTGCTAGAACCCGGTATAGTGGAAATTCCTGTATATTT 240
QY 250 TCAATATTAACAACATCATCTTCCGTCTTCTGCTCAATCTGTGGACAGCATTTCTATATGT 309
DB 241 TCAATATTAACAACATCATCTTCCGTCTTCTGCTCAATCTGTGGACAGCATTTCTATATGT 300
QY 310 GATTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGTTAAGTGAACGGGGTTGCA 369
DB 301 GATTAGTATCTATTAATTCGTAAGAGGTAGACGAGAGCGTTAAGTGAACGGGGTTGCA 360
QY 370 GATTTTGAAGGTGAATAGACTGCTTATCAAGTATTAATCTTATTAATCTTGAAGATTTG 429
DB 361 GATTTTGAAGGTGAATAGACTGCTTATCAAGTATTAATCTTATTAATCTTGAAGATTTG 420
QY 430 CTTACAGATTAATCAAAATCTTAATAAACTTGCTGAGTATTAACGTTCCAGACGG 489
DB 421 CTTACAGATTAATCAAAATCTTAATAAACTTGCTGAGTATTAACGTTCCAGACGG 480
QY 490 GAAGAAGATTTCACTAAATCTTTAGAGGGTCATTATCAAGACGAAAGCTGAATTTTA 549
DB 481 GAAGAAGATTTCACTAAATCTTTAGAGGGTCATTATCAAGACGAAAGCTGAATTTTA 540
QY 550 TTAATGCTTAAGTATGCAAGCTCAAAATGTGCAATTAATTAATTAAGGAGCGAGTT 609
DB 541 TTAATGCTTAAGTATGCAAGCTCAAAATGTGCAATTAATTAATTAAGGAGCGAGTT 600
QY 610 AATATTAATAAAGATGGGACTATGCTGTCACACCTGTTGATCCAGGGTCAGGAGAACT 669
DB 601 AATATTAATAAAGATGGGACTATGCTGTCACACCTGTTGATCCAGGGTCAGGAGAACT 660
```

```
QY 670 GATTTGAACGAGCGTTAAAGCGAAATTAAGAGTATTAATTAATTTGTTAGGCTGG 729
DB 661 GATTTGAACGAGCGTTAAAGCGAAATTAAGAGTATTAATTAATTTGTTAGGCTGG 720
QY 730 TATTAACAAGGTTTATAGATCAGATTAAGACAGCGGGTACAAAGTCTGAAGTTTGCGAAA 789
DB 721 TATTAACAAGGTTTATAGATCAGATTAAGACAGCGGGTACAAAGTCTGAAGTTTGCGAAA 780
QY 790 TTTTAATTAATTTGCTAGAGAAATGACCTTGCGGATTTGATTAATTTGCTATATTTCCA 849
DB 781 TTTTAATTAATTTGCTAGAGAAATGACCTTGCGGATTTGATTAATTTGCTATATTTCCA 840
QY 850 ACTTAATGATTTTGAATAATATCCATTAGCAACAAGTATGATTAATTAAGGAAATTTAT 909
DB 841 ACTTAATGATTTTGAATAATATCCATTAGCAACAAGTATGATTAATTAAGGAAATTTAT 900
QY 910 ACAGATCCAGTGGGATATTCAGGGGGAATTAATGCTGGGAACGGTTTATTAATGCTTAAAT 969
DB 901 ACAGATCCAGTGGGATATTCAGGGGGAATTAATGCTGGGAACGGTTTATTAATGCTTAAAT 960
QY 970 TCGGTAGAAAGCAATGGAACACGGGGAACCTGCTTATAGTTACTTGGCTTACACTATAGAT 1029
DB 961 TCGGTAGAAAGCAATGGAACACGGGGAACCTGCTTATAGTTACTTGGCTTACACTATAGAT 1020
QY 1030 ATATATAGTCAATCTATTAATCTTCAGCTTGTGTTATCTTATAGTGGCTGGGGGGAACCTGCT 1089
DB 1021 ATATATAGTCAATCTATTAATCTTCAGCTTGTGTTATCTTATAGTGGCTGGGGGGAACCTGCT 1080
QY 1090 CATTAATGAAGACTTCAACAAAGGTTAACGGTGTCTTTTCAACGATGCTTGGAACTACAGAT 1149
DB 1081 CATTAATGAAGACTTCAACAAAGGTTAACGGTGTCTTTTCAACGATGCTTGGAACTACAGAT 1140
QY 1150 AATTAATCCAGTAATATTTTGTGGCAATACCGATATATTTAATAATTTTCAATTAAGT 1209
DB 1141 AATTAATCCAGTAATATTTTGTGGCAATACCGATATATTTAATAATTTTCAATTAAGT 1200
QY 1210 AGATATGCAATCAACCGTTTGTGGGTAATCAATCCCAAGGATCTTGTTCACAGTGA 1269
DB 1201 AGATATGCAATCAACCGTTTGTGGGTAATCAATCCCAAGGATCTTGTTCACAGTGA 1260
QY 1270 GAATTTTTCGACAAACATTAATCTTCTGTATAGGTTAAACAGTTCTGGGTACTCA 1329
DB 1261 GAATTTTTCGACAAACATTAATCTTCTGTATAGGTTAAACAGTTCTGGGTACTCA 1320
QY 1330 CAGACAAATGAATCTGTGTTACAGGATTAATAAGATCTCACACTAGTGTGTAAT 1389
DB 1321 CAGACAAATGAATCTGTGTTACAGGATTAATAAGATCTCACACTAGTGTGTAAT 1380
QY 1390 TACTCTCATAGATTAATCAAAATGGGATGTTCAAAATGAACCTCCAGATTTAACGTA 1449
DB 1381 TACTCTCATAGATTAATCAAAATGGGATGTTCAAAATGAACCTCCAGATTTAACGTA 1440
QY 1450 TTTGTTTGACACATACAAAGTATGAATAAAGATTAATCGAATTTATCCAGATTAATTAAG 1509
DB 1441 TTTGTTTGACACATACAAAGTATGAATAAAGATTAATCGAATTTATCCAGATTAATTAAG 1500
QY 1510 CAATTTCTGCAATTAACCTTTGCTTACAGAGGTTACAGGATATGCAAGAGGTTAC 1569
DB 1501 CAATTTCTGCAATTAACCTTTGCTTACAGAGGTTACAGGATATGCAAGAGGTTAC 1560
QY 1570 GTACAGCTGGGCTGGTATTAACAGAGGAGATGTATACGTTACCTTATCAAGCAAGT 1629
DB 1561 GTACAGCTGGGCTGGTATTAACAGAGGAGATGTATACGTTACCTTATCAAGCAAGT 1620
QY 1630 TTAATAAATAGTTTAACTTCTGACCCACGAATTAATAATTAACGTTTGAATTCGCTTAC 1689
DB 1621 TTAATAAATAGTTTAACTTCTGACCCACGAATTAATAATTAACGTTTGAATTCGCTTAC 1680
QY 1690 GCGAGTGAAGGACCTGTGCTGTTCCGAGTGAAGAAAGTGTCCGCAAGTTCTGTTCAAT 1749
DB 1681 GCGAGTGAAGGACCTGTGCTGTTCCGAGTGAAGAAAGTGTCCGCAAGTTCTGTTCAAT 1740
QY 1750 GCTAATATTTTCTGCTCAGCTACAGGTGCTATAGTTCAATTTGATTAATGACACCTTA 1809
```


Db 1369 AGGATGACATTAATCTACGTTCCCACTGT-----ATTGCATCTAATGTGTAGA 1422
Qy 1387 AATTACTTCATAGATTATCAATATGCGCATGTGTTCAAAATGAACCTCCAGATTAC 1446
Db 1423 GGCCTCTCATATGATTATCAATATGCGCATGTGTTATATGAAATCCCAAGTTAAC 1482
Qy 1447 GATTGTGTGACACATACATATGAAAAAGATATGAAATTTATCCAGATTAAT 1506
Db 1483 GTATATGTGTGACATACATATGAAATGAAATGAAATTTATGAGCATCAAT 1542
Qy 1507 ACCCAATTCCTGCAAGTAAAGCTTTTGCCCTACCAAGCATGACAGATATGCAAGAGT 1566
Db 1543 ACACAAATACCGCGGGAAGATTATACCTTCAAAATATCTGTGTAATGCTATACC 1602
Qy 1567 TAGCTACAGCTGGGCT 1584
Db 1603 TATGTATTAAGGCACT 1620

RESULT 5
US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXM1-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
US-10-781-979-1

Query Match 37.0%; Score 747.2; DB 8; Length 5980;
Best Local Similarity 69.8%; Pred. No. 4,4e-165;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

Qy 1 GTGAAAAATATGAATCTTATCAAAATATCAAAATATGAATATGAATATTCGATGCTCCCG 60
Db 168 GTGAAAAATATGAATCTTATCAAAATATGAATATGAATATGAATATTCGATGCTCCCG 227
Qy 61 AATTAACAATATATGTCACAAACAGATATCTTTTGCAAGAGATCCAAATATATTTCTATT 120
Db 228 AATTAACAATATATGTCACAAACAGATATCTTTTGCAAGATATGCGGATATGCTACTATG 287
Qy 121 AACCTGAGCTGTGACGAGGAGCCATGCAAGATATCGTGGAAATAGCTCGAATATA 180
Db 288 TCTTGGATATATGTCAGGGAATCTCATGGAATGAATTTGGGAATAGTCGAAGCATATA 347
Qy 181 GTAATATTTGGAATATCTTATCAATATCTTGTGTAAGACCCGGATATGAGTGAATTCCT 240
Db 348 ACAAGATTTGGGAATATCTTATGAGTTGTGATTAACCTAGTTGGGTGGAATTAAT 407
Qy 241 GTATATTTTGAATATTAACAAATCATTTCCGCTTCTGTGTCATCTGTGACAGCATTT 300
Db 408 ACATATATCAATATTAAGAAAACTAATCCGACTATCGTCAAACTGTGACAGCATTT 467
Qy 301 TCTATATGATATTAATATCTATTAATCTGTAAGAGGTATACAGAGAGCGGTATTAAGTAC 360
Db 468 TCTATATGATATTAATATCTATTAATCTGTAAGAGGTATACAGAGAGCGGTATTAAGTAC 527
Qy 361 GGGGTTGCAATTTTGAAGGTGAAGATGATGCTTATCAAGATTAATCTTCAATATCTT 420

Db 528 GCGATTTGCAAGATTTTGAAGGTGAAGATTAATGAAGATTAATGAGATATATCTTCTATCTT 587
Qy 421 GAGATTTGGCTTACG-----ATAATCAATCTTAAATACTTGGTGCAC 465
Db 588 GGGGCTTGGCTTAAAGACGCTTAAACCACTTCAAAAGACAATAATTCGATATCGACACA 647
Qy 466 GTATGTTAAACAGTCCAGACACGGAAGAAGTTTCACTAACTTTTGAAGGTCATTA 525
Db 648 TTATGTTATTAATTTTAAACCTTTCAGAAAGAGTTTCAATGAATTTCTGAGAGGTCATTTG 707
Qy 526 TCAAGACAAAGCTGAATATTAATTTATTTGCTTACGATATGTCAGATGCAATATGAT 585
Db 708 TCAAGAAACAAATGCTCAAGATATTTTATTAATCTTTTGCACAAAGCTCAAAATGTCAG 767
Qy 586 TTATTAATTAATTAAGGACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 645
Db 768 TTATTAATTAATTAAGGACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 827
Qy 646 TTGTATCCAGGCTCAGGAGAA-----CTGATTTGT 675
Db 828 GAGATATGATGATCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 887
Qy 676 AACGAGCGGTTAAAGCGAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 735
Db 888 TATGAGCATTTAAATGCAAAACGCGACAGATATCAATTAATTTATTTATTTATGATACAG 947
Qy 736 AAGGTTTATGATCAATTAAGACAGCGGCTACAGTCTGAAATTTGCTCCAAATTTAT 795
Db 948 GTATGTTTAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1007
Qy 796 AATATTCGTAAGAAATGACGTTGGCGGATATGATTAATTAATTAATTAATTAATTAATTAAT 855
Db 1008 AATATTCGTAAGAAATGACGTTGGCGGATATGATTAATTAATTAATTAATTAATTAATTAAT 1067
Qy 856 GATTTTGAATAATATCATTTAGCAACAGTGTAGATTAATTAATTAATTAATTAATTAATTAAT 915
Db 1068 GATTTTGAATAATATCATTTAGCAACAGTGTAGATTAATTAATTAATTAATTAATTAATTAAT 1127
Qy 916 CCAATGGAATATTCAGGAGGAAATTAATGTTGGAAACGCTTT-----TTAGCTTTAT 969
Db 1128 GCAATGGAATATTCAGGAGGAAATTAATGTTGGTAATGCAATTTGCTTAATCTTTTAT 1187
Qy 970 TCGGTAGAAAGAAATGGAACAGGAGGAACTGTTTATGATTAATTAATTAATTAATTAATTAAT 1029
Db 1188 GGTATGAGGCTTAATGGAACAGGAGGAACTGTTTATGATTAATTAATTAATTAATTAATTAAT 1247
Qy 1030 ATATATGATCATTTCTATTAATCTTCAAGCTTGTATCTTATGAGCTGAGGAGGAACTGCT 1089
Db 1248 ATATATGATCATTTCTATTAATCTTCAAGCTTGTATCTTATGAGCTGAGGAGGAACTGCT 1298
Qy 1090 CATTAATGAAGATTCACAAAGGTTAACGCTTTTCAACGTAATGTCGAACTACAGAT 1149
Db 1299 CATTAATGAAGATTCACAAAGGTTAACGCTTTTCAACGTAATGTCGAACTACAGAT 1358
Qy 1150 AATTAATCCAGTAATTAATTTTGGCAATACGATATTAATTAATTAATTAATTAATTAATTAAT 1209
Db 1359 AATTAATCCAGTAATTAATTTTGGCAATACGATATTAATTAATTAATTAATTAATTAATTAAT 1418
Qy 1210 AGATATGCAATCAACCGTTTGTGGTATTAATCAATCCACGAGCATCTTGTTCACGTCGA 1269
Db 1419 A---TCATGAACCTGTAAGAGAGACCTACCGTACAGCAAGATATGCTTCAAAAGCA 1475
Qy 1270 GAATTTTTCGACAACTAAATATCTTCTGTAATGAGTAAACAGTTCTGGG---TAC 1326
Db 1476 GAATTTTTCGACAACTAAATATCTTCTGTAATGAGTAAATGAGTAAATGAGTAAATGAGTAA 1535
Qy 1327 TCACAGACAATTAATGATGCTGTTTACAGGTATTAATTAATGAGTAAATGAGTAAATGAGTAA 1386
Db 1536 AGGATGACAATTAATGATGCTGTTTACAGGTATTAATTAATGAGTAAATGAGTAAATGAGTAA 1589
Qy 1387 AATTAATCTCAATGATTAATCAATGCGGATGTTCAAAATGAACCTCCAGAGTTAAC 1446

```
Db 1590 GGACCTCTCATAGATTATCAATGCGGCATGTGTGTATGAGAACTCCAGACTTAC 1649
Qy 1447 GTATTGGTTGACACATACAGTATGAAAAAGATAATTCGATTTCAGATPAAATT 1506
Db 1550 GTATATGGTTGACACATACAGTATGAAAAAGTGAATAATATGAAAGCAATCAATT 1709
Qy 1507 ACGGAATTCCTGAGTAAGACCTTTGGCTTACACAGAGTACAGATATGACAGAGT 1566
Db 1710 ACACAAATACCGGCGGAGAGATTATTAATCTTCAAAATTAATCTTGTAAATGCTTATACC 1769
Qy 1567 TACGTACAGCTGGGACCT 1584
Db 1770 TATGTATTAATAAGGCACT 1787

RESULT 6
US-10-781-979-4
; Sequence 4, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: MM1-008, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for its use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781.979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2073)
US-10-781-979-4

Query Match 36.6%; Score 739.8; DB 8; Length 2073;
Best Local Similarity 69.7%; Pred. No. 1.4e-163;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;

Qy 10 ATGAATCTTATCAAAATATCAAAATGATATGAAATTCGTGATGGTCCCGAATAACACA 69
Db 1 ATGAGTCCATATCAAAATATCAAAATGATATGAAATTCGTGATGGTCCCGAATAACACA 60
Qy 70 AATATGCAAAAGATATCTTTTGGCAAGGATCCAAATATATTTCTTATTAACCTGAGC 129
Db 61 AATAGCGCAAAAGATATCTTTTGGCAAAATATGCGGATATGTTACTATGTCTTGAAT 120
Qy 130 GCTTGTACGGAGGCGCATGCGCAAGATACGTGGGAATCAGTCTCGAATATGTAATTT 189
Db 121 GATTGTACGGGAATCTCATGGATGAAATTTGGGAATCAGCGCAAAAGATPAAAGATTT 180
Qy 190 GGGACATACCTTATACAAATCTTGCTAGAACCCGGTATAGTGAATTCCTGTATATTTT 249
Db 181 GGGATTAATCTTATAGAGTTGTGTAGAACCTTAGTTGGTGAATTAATACCTATTA 240
Qy 250 TCAATATTAACAACAATCATTCCTGCTTGTGTCATCTGTGGACGACTTCTATATGT 309
Db 241 TCATATATAGGAAACCTAATTCGACTATGTCAAACTGTGTACGACACTTCTATATGT 300
Qy 310 GATTATGATCTATTAATTTGTAAGAGGTAGACAGACGTTTAAGTGAACGGGGTTGCA 369
Db 301 GATTATATCTATTAATTTGTAAGAGGTAGACGATAGTGTTTTAAGTGAATGCGATTGCA 360
Qy 370 GATTTGAAGGTGAATGACGCTTATCAAGATTATATCTTCAATTATCTTGAAGATTGG 429
Db 361 GATTTGAAGGTGAATGAAATTAATATAGAGATTATATCTTCTTATCTTTGGGCTTGG 420
Qy 430 CTTACAG-----ATPAATCAAATCTTAAAAAACCTTGCTGACGTAGTAA 474
Db 421 CTTAAAGACGGTAAACACATTCAAAAGACAAATTAATCTGTATATCGGCAATAGTTAT 480
Qy 475 CAGTTCCAGACGGGAAAGAAATTTACTTAATCTTTAGCAGGGTCAATTATCAAGAC 534
Db 481 TATTTTAACTTTCAAGAAAGATTCAGAAATTCAGAGGGGTCAATGTCAAGAAC 540
Qy 535 AAAGCTGAATATATATATGCTAGATGTCAGACCTGCAATGNCATTTATTTCTA 594
Db 541 AATGCTCAAGTATTTTATTTACTTCTTTTGCACACAGCTGCAATGTCGTTATCTA 600
Qy 595 TTAAGGACCGAGTTAATATTAATAAAGAAATGGGACCTAGTGTCCACCGTTTATCCA 654
Db 601 TTAAGGATGACAGTTCAATATTAAGACAAATGTTCCATTTTGAATGACAGAAATGTA 660
Qy 655 GGGTCAGGAGAA-----CTGATTTGACAGCGG 684
Db 661 AGATCGGAATTAATATACCTAACAGTGTGTGATTTTACCGGTGATTTACTATAGACGA 720
Qy 685 TTAAGACGAAATTAAGAAGTACTAATTTATTTGTAGGGGTATTAACAAGGTTTA 744
Db 721 TTAATATGCAAAACGCGAGATATCAAAATATTTGTTATATGATACAGTAGTTTA 780
Qy 745 GATCAGATTAAGACAGCGGGTACAGTGTGAAATTTGTCGAAATTTAAATTAATTCGT 804
Db 781 AATCAGATTAAGACAGCGGGGACAGGCTGACAGCTTGTCGAAATTTAAATTAATTCGT 840
Qy 805 AGGAAATGACGTTGGCGGTATGATATTAATTTGCTATATTTCCAACTTATGATTTGAA 864
Db 841 AGGAAATGACGTTGGCGGTATGATATTAATTTGCTATATTTCCAACTTATGATTTGAG 900
Qy 865 AAATATCCATTAAGCAAAAGTATAGTTAACTTAAAGGAAATTTATACAGTCCAGTGA 924
Db 901 AAATATCCATTTGCCAACAATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Qy 925 TATTCAGGGGAAATTTATGTTGGGAAAGGTTTT-----TTAGCTTAAATTCGTGAA 978
Db 961 TATTCATCGGGAATTTATGTTGGTTCGGAATTTGCGTAATCTTTTAAATGGTTAGG 1020
Qy 979 GCAATGGAACACGGGACCTGTTAGTACTTGTGCTTCAAGCTATAGATATATATAGT 1038
Db 1021 GCTAATGGAACACGGGACCTGTTAGTACTTGTGCTTCAAGAAATTTAGTATATATAT 1080
Qy 1039 CATTTATTAATCTTACGTTGTGTATCTTAGTGGCTGGGGGGAATCTGCTATTAAGA 1098
Db 1081 GAGTATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGAATCTGCTATTAAGA 1131
Qy 1099 GACTTCAAAAGGTAACGGTGTCTTCAAGTATGCTGGAACCTACGATTAATATCCA 1158
Db 1132 GACTTCAAAAGGTAACGGTATATTTTCAACGATATGCTGGAACCTACGATTAATATCCA 1191
Qy 1159 GCTAATTAATTTTGGCAATACCGATATATTAATTAATTTCAATTTAGCTAATATGA 1218
Db 1192 GCTAATTAATTTTGGCAATACCGATATATTAATTAATTTCAATTTAGCTAATATGA 1248
Qy 1219 ATGCAACCGTTGTGGGTATTCATCCACCGCACTGTTTCACTGAGAAATTTT 1278
Db 1249 AACCTAGTAGAAGACTACCGCTAGACAGAGTATGTTTCAAAAGGACGATTTTGT 1308
Qy 1279 CCGACAACACTAAATATCTTCTGTAATGAGTAAACAGTTCTGGG--TACTCAACAGCA 1335
Db 1309 AGGGTAGGGGACCTGATTTAAATTAATGATGAGGTATTAATGGGCTAACAGAGATGA 1368
Qy 1336 ATGGAATCTGTGTACAGGTATTAATAGAGTCTACACCTTATGCTTAACTTCT 1395
Db 1369 AATGAATCTAGCTTCCACTTGT-----ATTGACCTTAATGTTGTATAGAGACCTCT 1422
Qy 1396 CATAGATTAATCAATGCGGAGTGTCAAAATGAACCTCGAGATTAAGTATTTGTT 1455
Db 1423 CATAGATTAATCAATGCGGAGTGTGTATATGAAACTCCAGATTTAAGTATATGTT 1482
```

Oy	1456	TGGACACTACAAAGATATGAAAAAGATATGCGATTTATCCAGTATTAATACCAAT	1515
Db	1483	TGGACACTACAAAGTTTAAACGTAAATATTAATGAACCATCAATTCACAAATA	1542
Oy	1516	CCTCAGTAAAAAGCTTTGCCCTACACAGAGTACAGATTTGCAGAGGTTACGTACA	1575
Db	1543	CCGGGGGAGAAAGATTTACTCTTCAAAATATCTTGCTAAAGCTATACCTATGTATA	1602
Oy	1576	GCTGGGCGCT	1584
Db	1603	AAAGGCACT	1611

RESULT 7

```

US-10-099-285-71
: Sequence 71, Application US/10099285
: Publication No. US20030105319A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Schaeff, H. Ernest
:
: Wicker, Carol
: Narva, Kenneth E.
: Walz, Michelle
: Stockhoff, Brian
: Muller-Cohn, Judy
:
: TITLE OF INVENTION: Toxins Active Against Pests
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/099,285
: FILING DATE: 15-Mar-2002
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/002,285
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: APPLICATION NUMBER: US 08/674,002
: FILING DATE: 1-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sanders, Jay M.
: REGISTRATION NUMBER: 39,355
: REFERENCE/DOCKET NUMBER: MA-701C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5880
:
: INFORMATION FOR SEQ ID NO: 71:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3471 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 71:
:
US-10-099-285-71

```

	Query Match	8.5%	Score 172.4;	DB 5;	Length 3471;
	Best Local Similarity	54.2%;	Pred. No. 1.1e-29;		
	Matches	440;	Mismatches 336;	Indels	36; Gaps 3;
Cy	161	GGGATCTAGTCTCGGATATACGACTATTGGGACATACCCTTAATACAACTTCCTGTGAAC	220		

Db	158	GGATATGCAGAAAAGAACGATATCTATTGGGACACACATAGTCTCTTATACAGCAG	217
Qy	221	CCGGTATAGGTGGAAATTCCTGTAATATTTT-----CAATAATAAACAACATCTCCGT	274
Db	218	CTTCTCTTACGGATTAATTTCAATAGATATATAGACCTTAATAGTAAAGTACAGAGATA	277
Qy	275	CTTCGTGCATCTGTGGAGACACTTTCATATGTGTGATTTAGTATCTATATATTCGTAAAG	334
Db	278	GTATGGCAATTCATATCAGATTGTGCTATATGTGACCTTATATCTATATTAATGATTTAC	337
Qy	335	AGGTAGACGAGAGCGTGTAAAGTGCAGGCGGTGCAGATTTTGGAGTGAATGACTGCTT	394
Db	338	GGGTAAATCAGAGTGTTTTAAATGATGGATTTGACGATTTTATGGTCTGTACTCTTAT	397
Qy	395	ATCAAGATTAATATCTTC-----ATTATCTTGAAGATTGGCTTACAGATA	439
Db	398	ACAGAGACTATTTTAGAGCTCTGTATAGCTGTGAATATAGAAATCTTAATTCGTCTTGCTG	457
Qy	440	AATCAATATCTTAAATAAACTTGCTGACGTATGTTAAACAGTCCAGACACGGAAGAAGATT	499
Db	458	AAGAACTCCGATCTGTTTGTAGAAATCCCGACTCAGAAATTTATAGAAATTTTAAACCGAG	517
Qy	500	TCACTTAACTTTTAGCAGGGTCTATTATCAAGA CAGAAAAGCTGAAATATTTATATGCTTA	559
Db	518	GGCTTTTAAAGAAATGTGGCTGTAGCTAGACAAATATGCCAAATATATATTATTCCTT	577
Qy	550	CGTATGTGCAGCTCCCAATATGTGCATTTATTTCTATTTAAGGACGCACTTAATATATATAA	619
Db	578	CTTTTGCAGCGCTCAATTTTTCATTTATATTACTTAATAAGGATGCTACTAGATTAATGCA	637
Qy	620	AAGATGGGGACTAGTGTGTCCACCGTGTATCCAGGGGCAGGGAGAACTGATTTGTAAAG	679
Db	638	CTAATTTGGGGGCTATACATGCTACACCTTTTATATA-----ATTATCAAT	682
Qy	680	AGCGGTTAAAGCGGAAATTAAGAATATCTAATTAATTTGTGTAGGGTGTATTAACAAG	739
Db	683	CAAACTGTAGAGCTTATTTGAATATATCTATGATTTATGGCTACATGTGTATATCGAG	742
Qy	740	GTTTAGATCAGATTAAGACAGGCGGGGTACAAGTGTCTGAGCTTTGGTGCAAATTTAATAAT	799
Db	743	GTTCCTAAAGAACTTAAGACACAGAGCACATAGTCTCAAGCTTGTTAGATTTCAATAGAT	802
Qy	800	TTCTGAGAGAAATGAGTGTGGCGGATTTGAGATTAATTCATATATTTCCACCTATAGATT	859
Db	803	ATCTGAGAGAGATGCAATTTGATGTATTAAGATTAATGACATCAATTTTCAAGCTTGAATA	862
Qy	860	TTGAAAAATATCTATTAGCAACAAGTGTAGAGTTTAACTAGGAAATTTTATACAGATCCAG	919
Db	863	TTACTAATTAACCAATAGAAAACAGATTTTCAGTTGATGTGGGTCAATTTATACAGATCCAA	922
Qy	920	TGGATATTCAGGGGGAATTTATGTTGGGA	951
Db	923	TTGTTTTGTATCATGTAGTAGTCTTAAAGGA	954

RESULT 8

```

US-10-428-961-29
/ Sequence 29, Application US/10428961
/ Publication No. US20030237111A1
/ GENERAL INFORMATION:
/ APPLICANT: Baum, James A.
/ APPLICANT: Chu, Chih-Rel
/ APPLICANT: Donovan, William P.
/ APPLICANT: Gilmer, Amy J.
/ APPLICANT: Rupa, Mark J.
/ TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
/ TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
/ FILE REFERENCE: MECO201--1
/ CURRENT APPLICATION NUMBER: US/10/428,961
/ PRIOR APPLICATION NUMBER: 2003-05-02
/ PRIOR APPLICATION NUMBER: 09/661,322
/ PRIOR FILING DATE: 2000-09-13
/ PRIOR APPLICATION NUMBER: 60/153,995
/

```


PRIOR FILING DATE: 1999-09-15
 : NUMBER OF SEQ ID NOS: 63
 : SOFTWARE: Patentin version 3.2
 : SEQ ID NO 29
 : LENGTH: 2407
 : TYPE: DNA
 : ORGANISM: *Bacillus thuringiensis*
 US-10-428-961-29

Query Match 8.1%; Score 162.8; DB 6; Length 2407;
 Best Local Similarity 53.4%; Pred. No. 1.7e-27;
 Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

```

Qy 161 GGGATCACTCTCGATTAAGTAACTATGAGCAATACCTTATCAATCTTGTGTAAGC 220
Db 158 GCGATGACGAAAGAGCAGTATCTATTGGACAAACCATAGTCTCTTATCAACAGAC 217
Qy 221 CCGGTATAGTGAATCTGTATATTTT-----CAATATAACCAACTCATTCCT 274
Db 218 CTTCTCTTACTGATTAATTCAATAGTATATGACCTTATAGTAAAGTACTAGAGGTA 277
Qy 275 CTTCTGTCAATCTGTGACAGCATTCTATATGATTAATTAATTAATTTGTAAG 334
Db 278 GTAGTGGACATCAATACATATGATTTGTCTATATGACTTATATCTATTATGATTTAC 337
Qy 335 AGGTAGACGAGCGGTGTTAAGTACGCGGTTGCAATTTTGAAGGTAATGACTGCTT 394
Db 338 GGGTACATCAGAGGTTTAAATGATGGATGCAATTTTAATGTTTCTGTACTCTTAT 397
Qy 395 ATCAAGATTATATCTTC-----ATTATCTGAGATTTGCTTACATA 439
Db 398 ACAGAACTATTAGAGGCTCTGATAGCTGAATTAAGAACTTAATCTGCTTCTG 457
Qy 440 AATCAATCTTAAAAAACTTGCTGACGATGTTAAACAGTTCAAGCAAGGAGAAAGATT 499
Db 458 AAGAACTCCGACTCGTTTATGAAATCCGCACTGAAATTTGATAGATTTTAAACCGAG 517
Qy 500 TCACTAACTTTTACAGGGCTATTATCAAGACAAAGCTGAATATTTATTTATGCTTA 559
Db 518 GGTCTTAAAGAAATGATGGCTCGTTAGTACAGCAAAATGCCAAATATTTATTACTT 577
Qy 560 CGTATGTCAGAGCTGCAATATGATGATTTATTAATTAAGGACGCGTTAATATATAA 619
Db 578 CTTTGGAGCGCTGCAATTTTCCATTATTAATCACTAAGGATCTAATAGATATGCA 637
Qy 620 AAGATGGGACATAGTGTGTCACCGTTGATCCAGGGTCAGGGAATGATGTAAAG 679
Db 638 CTAAATGGGGCTATACAAATGCTACACCTTTATA-----ATTATCAAT 682
Qy 680 AGCGTTTAAAGCGAAATTAAGAGTATATTAATTTATGATGGGTGATTAACAGG 739
Db 683 CAAAATAGTAGAGCTTATGAATATATGATATTTGGGTATTTGGGATTAATGAG 742
Qy 740 GTTTAGATCAGATTAAGCAGCGGCTACAGTGTGAAGTTTGGTCAAAATTAATAAT 799
Db 743 GTTCAACCGAATTAAGCAAGAGGCGCTAGTGTCTAAGCTGTGTAATTCATGAT 802
Qy 800 TTGCTAGAGAAATGACCTGGCGGTATTTGATATTATTTGATTTTCAACTATGAT 859
Db 803 ATCGAGAGAGATACATTTATGAGGATTTAAGAAATAGTACATCTTTCAAGCTTATA 862
Qy 860 TTGAAAAATATCCATTAGCAACAAGTATAGTATAGTAAAGTAAATTTATACAGATCAG 919
Db 863 TTACTAATTTACCAATAGAAAAGATTTTCAGTTGATGAGGTCATTTATACAGATCCA 922
Qy 920 TGGGATATTCAGGGGGAATTTATGTTGGGA 951
Db 923 TTGTTTGTACATGATGATGATCTTTAGGGA 954

```

RESULT 9
 US-10-929-754-4
 ; Sequence 4, Application US/10929754

Publication No. US20050124803A1
 : GENERAL INFORMATION:
 : APPLICANT: ABDULLAH, MODH AMIR
 : APPLICANT: DEAN, DONALD H.
 : TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
 : FILE REFERENCE: 22727/04179
 : CURRENT APPLICATION NUMBER: US/10/929,754
 : PRIOR FILING DATE: 2004-08-30
 : PRIOR APPLICATION NUMBER: 60/498,826
 : NUMBER OF SEQ ID NOS: 43
 : SOFTWARE: Patentin Ver. 3.2
 : SEQ ID NO 4
 : LENGTH: 4391
 : TYPE: DNA
 : ORGANISM: *Bacillus thuringiensis*
 US-10-929-754-4

Query Match 6.6%; Score 133.6; DB 9; Length 4391;
 Best Local Similarity 48.1%; Pred. No. 1.8e-20;
 Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;

```

Qy 540 TGAATATTTATTTGCTACGTATGTCAGACGTCGAATGTCATTTATTTACTATTAG 599
Db 1303 TGAATTAATTTATTTGCTGCTGATGACAAATTTGCAATCTGATTTACTTTATTAACG 1362
Qy 600 GGAAGCAGTTAAATATTAATAAGATGGGAGTATGTCACACCGTTGATCCAGGGTC 659
Db 1363 GGAATCTCAATTTATGAGATTAATGATGAGCGCACG-----AGCTAA 1407
Qy 660 AGGAGAACTGATTTATGACAGCGGTTAAAGCGAAATTAAGATTAATTAATTTG 719
Db 1408 TGCTCGATTAATTTATTAACCAATATTAAGAAATTAAGAAATTAAGAAATTAAG 1467
Qy 720 TGTAGGTGATTAACAGGCTTTATGATGATTAAGCAGCGGGTCAAGTCTGAAT 779
Db 1468 TATTAATTTGATTAATTAAGGTTTAAATGATTTTGAACAGCAGTCA----- 1516
Qy 780 TTGTCGAATTTAATTAATTTGTCGAGAAATGACGTTGCGGTATTTGATTAATTTG 839
Db 1517 -TGGGTAACTTTAATTCGTTATGTCGAGAAATGACCTTACTGATTAATTAATTTT 1575
Qy 840 TATATTTCCACTATGATTTTGAATAATTCATTAAGCAACAAGTATAGTAACTAG 899
Db 1576 AATGTTCCCTATTATTAAGACGAGATTAATTCCTAAGAAATTAAGAAATTAAG 1635
Qy 900 GGAATTTATACGATTCAGTGGATTTTCAAGGGGAAATTAATGCTTGGGAAGGTTTT 959
Db 1636 GGAATTTATTCAGT---GTATTTAATGGGAGATTAATGACCTTATGATCTCTTATTT 1692
Qy 960 TAGCTTAATTCGTTAAGCAATGGAACAGCGGGACCTGTTAGTTTACTTGGCTTCA 1019
Db 1693 TTTCTTTGAGAAAGCTGAATCACTTTATTAAGAGGACCCCATCTCTTCACTTGGCTAAA 1752
Qy 1020 AGCTATAGATTAATTAATGATCTATTAATCTTCAAGCTTGTATCTTATGAGCTGGGG 1079
Db 1753 AGATTTGATTTGTAACCAATTTCTATTCTTATTTGGAATTTTATACAGTGTGCAAA 1812
Qy 1080 GGAACCTCGCATTTATGAAGATCTTCAAAAGGTAACGCTGCTTTCAACGATATGCTGG 1139
Db 1813 TAAGTATCTTAATCAATTAATTTCTAGTATTAACGAGGCTCTTTTAAAGGGAACAGGAC 1872
Qy 1140 AACTACGAGTAATTAATCAAGTAATTTATTTT-----GGCAATACGATTAATTTAAAT 1196
Db 1873 AGATTAATGAGGAGCTTTCTTCACTTAATTAATTTCAATCAATTTCAATTAATTTT 1392
Qy 1197 TATTTCAATTAAGTATGATGATGCAACCGTTTGTGGTATCA---ATCCACGGCA 1253
Db 1933 ATGACGGAATAATTAATTAATTAATTTATCTTGGGATGATCTGTAATTAATTAATAAAT 1992
Qy 1254 TCTTGTTCACGTCGAGATTTTTCGCAACACTAATTAATCTTCTGATAGAGTTAA 1313
Db 1993 GAATTTTCTGTAACAGATTAATTAATTTCTCAAAAGATTAATTAATTAATGTCACAGAAC 2052

```


Query Match 5.8%; Score 117.6; DB 8; Length 1806;
 Best Local Similarity 46.6%; Pred. No. 6.8e-17;
 Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 406 TATCTTCATTTATCTTGGAGATTGGCTTACAGATTAATCAAACTCTAAATACTTGCTGAC 465
 DB 310 TATATCAATTTAGTATGATGATGGAAAATGATTTGAAAATCTCAAGGCTCAAGATGAG 369
 QY 466 GTAGTTAAACAGTTCCAGACCGGAAAGAAATTTCACTAACTTTTGAAGGCTCATTA 525
 DB 370 GTAGCTAATTACTATGAAAGCTTGAGCAGCGGTTGAAAGAGTATGCC---TCAATTT 426
 QY 526 TCAAGACAGAAAGCTGAATATTTATTTGCTTACGATGATGCAAGCTGCAATATGCAAT 585
 DB 427 GCAGTGAAGATTTTGAAGTACCACTTTTAACTGTCTATGTGCAAGCTGCTAAATCTTCAT 486
 QY 586 TTATTTACTATTTAAGGACGACGATTAATTAATAAAAGATGGGACATGATGTGTCACCG 645
 DB 487 TTATTTATTTAAGAGATGTTTCACTTATGAGAAAGTGTGGGA-----531
 QY 646 TTGTATCCAGGCTCAGGAGAACTGATTTGTAACGAGCGTTAAAGCGAAATTAAGAG 705
 DB 532 TGGTCGAGCAGAAAATTTAAATTTATGATTAACAGATTAA---GTAATCCATGAA 588
 QY 706 TATATCTAATTTATGTGATGAGGTGTTATACAGGCTTTAGATCAGATTAACAGCGGCGT 765
 DB 589 TACACAAATCATTTGTGTAATTTGTTAATAAAGAGCTTAAGATTAATAAATTAAGGT 648
 QY 766 ACAAGTCTGAAGTTTGGTGGAAAATTTAATAAATTTGTAAGAAATGATGCTGGCGGTA 825
 DB 649 TCTTTCTTATCAAGATTTGTAATTAATTCGTTTCCGTGAGAAATGATCTTACTGTT 708
 QY 826 TTGATATTTATGCTATATTTTCCAACTTATGATTTTGAATAATTCATTAAGCAACAGT 885
 DB 709 TTAGATATCGTGGCTTATATCCGCACTATGATGTAACAACTATCCAAATTAACCGGT 768
 QY 886 GTAGAGTTAATCTAGGAAATTTATACAGATTCAGTGGGATTTTCAAGGGGAAAT---AT 942
 DB 769 GCTCAGCTAACAGGGAAGTTTATACGATCTTTACTTAATTTTAACTTAAATTAATCAT 828
 QY 943 GGTGGGAACGTTTTTTTAACTTTAATTCGTGAGAACCAATGGAACACGGGACCTGCT 1002
 DB 829 TCTGTGCTCAATTTACTTATTTTGAACATGAGAAATGCAACATTAAGACCTCCACAT 888
 QY 1003 TTAGTTACTTGGCTTCAAGCTATGATATATATATGATTTCTATTAATCTTCAAGCTTGT 1062
 DB 889 CTGATGGAATTTTAAAGATGCTAACAAATTTATACAGATTGATGTGAGGAAGAAC 948
 QY 1063 TATCTTAGTGGCTGGGGGGAACCTGCTATTAAGAGATTTCAACAAAGGTTAACGGTCT 1122
 DB 949 TATTTATGGGAGAGACATTCGCTGACCTCTTACATGAGAGAGAGAAATATTAAGATCA 1008
 QY 1123 TTTCAACGTAATGCTGGAATCAAGATTAATCAACGTAATTTATTTTGGCAATACC 1182
 DB 1009 CCTCTATATGATGAGAGGCAATCAAGAGGTTCTTAAGAGATTTTATTTTATGACACC 1068
 QY 1183 GATATATTTTAAATTTATTTCAATAGCTAGATATGCAATGCAACGTTTGTGGGATTTCA 1242
 DB 1069 GTTTTAAAGCGTTATCAAGCGGACCTTAAGACCAATTAACAGACGCTGACACAGCTCCT 1128
 QY 1243 ATCCACGCGATCTTGTTCAGCTGAGAAATTTTCCGCAACACTAAATTTACTTCTG 1302
 DB 1129 CCTTTAATTTAAGTACTTGAAGGAGTGAATTTCCACACTCTTACAGGATGATTTTATG 1188
 QY 1303 TATAGGTTAAACGTTCTGGGTACTCAGACAAATTAATCTGATGTTTACAGGATTAAT 1362
 DB 1189 TATCTGTAAGAGAGATGCTAGATTTCTTTATATGATGCTCCGCTTTTAACTCCAGTTGG 1248
 QY 1363 AAGATCTACACCTAGCTGTAACAAATTTACTTCTATGATTAATCAATGCGGACATGTT 1422
 DB 1249 TTACTCTATAGGATATACAGTCCGTTTATGTCATGCAACGTTTGTGTTAATCTGGG 1308
 QY 1423 CAAATGAAACCTCCAGAGTTAAGTATTTGTTGGACACATACAGATTAAGAAAAAGAT 1482

DB 1309 ACCCTTATTTAAACAGGTGCAATCTTTTCTTGACACATGATGTCTGAAGAAC 1368
 QY 1483 AATGAAATTTATCCAGATTAATAATTAACGCAAAATCTGCAATTAAGGCTTGTGCTACCA 1542
 DB 1369 AATACAAATGAAATCAAAATTTATTAACGAAATCCGTTAGTAAAGCATATCAAAATTTGG 1428
 QY 1543 GCAGGTAC 1550
 DB 1429 TCAGGCAC 1436

RESULT 12
 US-10-782-020-2
 ; Sequence 2, Application US/10782020
 ; Publication No. US20040197916A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carozzi, Nadine
 ; APPLICANT: Hargis, Tracy
 ; APPLICANT: Koziel, Michael G.
 ; APPLICANT: Duck, Michael B.
 ; APPLICANT: Carr, Brian
 ; TITLE OF INVENTION: AXMT-004, A Delta-Endotoxin Gene and
 ; TITLE OF INVENTION: Methods for Its Use
 ; FILE REFERENCE: 045600/274139
 ; CURRENT APPLICATION NUMBER: US/10/782,020
 ; CURRENT FILING DATE: 2004-02-19
 ; PRIOR APPLICATION NUMBER: 60/448,810
 ; PRIOR FILING DATE: 2003-02-20
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1890
 ; TYPE: DNA
 ; ORGANISM: *Bacillus thuringiensis*
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1890)
 US-10-782-020-2

Query Match 5.8%; Score 117.6; DB 8; Length 1890;
 Best Local Similarity 46.6%; Pred. No. 6.9e-17;
 Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 406 TATCTTCATTTATCTTGGAGATTGGCTTACAGATTAATCAAACTCTAAATACTTGCTGAC 465
 DB 394 TATATCAATTTAGTATGATGATGGAAAATGATTTGAAAATCTCAAGGCTCAAGATGAG 453
 QY 466 GTAGTTAAACAGTTCCAGACCGGAAAGAAATTTCACTTAATCTTTTGAAGGCTCATTA 525
 DB 454 GTAGCTAATTACTATGAAAGTCTTGAAGCGGCTTGAAGAGAGATATGCC---TCAATTT 510
 QY 526 TCAAGACAGAAAGCTGAATATTTATTTATTTGCTAGCTATGCAAGCTGCAATATGCAAT 585
 DB 511 GCAGTGAAGATTTTGAAGTACCACTTTTAACTGTCTATGTGCAAGCTGCTAAATCTTCAT 570
 QY 586 TTATTTACTATTTAAGGACCACTGATTAATTAATAAAGAAATGGGCACTAGTGTGTCACCG 645
 DB 571 TTATTTATTTAAGAGATGTTTCACTTATGAGAAAGTGTGGGA-----615
 QY 646 TTGTATCCAGGCTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGAG 705
 DB 616 TGGTCGAGACAGAAAATTTAAATTTTATGATTAACAGATTAA---GTAATCCCATGAA 672
 QY 706 TATCTAATTTATTTGCTAGGCTGATTAACAGGCTTTTATGATGATTAAGACAGGCGGT 765
 DB 673 TACACAAATCATTTGTATTAATTTGTTAATAAAGACTTGAAGATTAATAAATTAAGGT 732
 QY 766 ACAAGTCTGAAGTTTGTGCAATTTAATAATTTGTAAGAAATGACGTTGGCGGTA 825
 DB 733 TCTTTCTTATCAAGATTTGTAATTAATTTATGCTGTTCCGTAAGAAATGACCTTACTGTT 792
 QY 826 TTGATATTTATTTGCTATATTTTCCAACTTATGATTTTGAATAAATATCATTAAGCAACAGT 885

Db 1633 TTACCTCATAGGATACAGTACCGTTTATGTCATGCAACGTTTGTCTTAATTCGG 1692
QY 1423 CAAATGAAACCTCCAGAGTTAACTGTTGGTGGACACATACAGTATGAAAAAGAT 1482
Db 1693 ACCCTTATTTAAACAAGGCGCATCTTTCTTGGACACATCGTATGCGTGAAGAAC 1752
QY 1483 AATGGAATTTATCCAGATTAATTAAGCAAAATTCCTGCAAGTAAAGCTTTTCCCTAAC 1542
Db 1753 AATACAAATGGAATCAATATATATATACCAATCCGTTAGTAAAGCATATCAAAATGGG 1812
QY 1543 GCAGGTAC 1550
Db 1813 TCAGGCAC 1820

RESULT 14

US-10-428-961-62
; Sequence 62, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Jiah-Red
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-62

Query Match 5.8%; Score 116.8; DB 6; Length 3684;
Best Local Similarity 55.0%; Pred. No. 1.5e-16;
Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;

QY 406 TATCTTCATATCTTGGAGATTGGCTTACAGATTAATCAATCTTAATAAATCTTGCTGAC 465
Db 400 TATCAACAGTCACCTTGAAGATGGCTAGAAAAACCGTATGATGCAAGAACGAGAGGTG 459
QY 466 GTAAGTAAACAGTTCCAGACCGGAGAGAGATTTCCTAACTTTAGCAGGTCATTA 525
Db 460 CTTTATATCCATATATAGCTTGAAGCTTGAATTTCTTAATGGAGATCCGCTTTTGCA 519
QY 526 TCAAGACAGAAAGCTGAATATTTATTTATTTCTTACGATGTGCAAGCTGCAAAATGTCAT 585
Db 520 ATTAGAAACCAAGATTCATATATATG---GTATATGCTCAAGCTGCAAAATTTATCAC 576
QY 586 TTTATTTACTATTAAGGACGACGATTAATTAATAAAGAAATGGGACATGATGTGCCACG 645
Db 577 CTATTTATTTATGAGATGCTCTCTTTTGGTAGTAATTTGGGCTTACATCCCAAGAA 636
QY 646 TTGTATCCAGGTCAGGAGAACTGATTTGAACGAGCGGTTAAAGGAAATTAAGAG 705
Db 637 ATTCAACG-----TTATTTAGAGGCCAAGTGAAGAAAGAGAGAA 678
QY 706 TATATCTAATTTATGTTAGGTTGATTAACAAGGTTTAATCATCATTAAGACAGGCGGT 765
Db 679 TATTCGATTAATTTAGCGCAAGATGATTAATACGGGTTTAATTAATTTAGAGAG-----GGG 732
QY 766 ACAAGTCTGAAGTTTGGTGAATTTAATTAATTTGATGAGAAATGAGAGGTTGGCGGTA 825

Db 733 ACAAGTCTGAAGTTGTTGGATTAATTAATCAATTCCTGAGAGCTTAACGTAAGAGTA 792
QY 826 TTGATATATTTATGCTATATTTCCAACTTATGATTTGAAAAATTCATTAAGCAACAGT 885
Db 793 TTGATCTAGTGCACATTTCCAGAGTATGACACGCGTGTATTTATCCAAATGAATACAGT 852
QY 886 GTAGAGTTAACTGAGGAATTTATACAGATCCAGTGGATATTCAGGGGAAATTAATGT 945
Db 853 GCTCAATTAACAAGAAATTTATACAGATCAATGAGGAGAAATGACACCTTCAGGA 912
QY 946 TGGGAACGTTTGTAGCTTAAT 969
Db 913 TTGCAAGTACGAATGTTTAAT 936

RESULT 15

US-10-665-460A-7
; Sequence 7, Application US/10665460A
; Publication No. US20040096934A1
; GENERAL INFORMATION:
; APPLICANT: Freysinet, Georges
; APPLICANT: Rang, Cecile
; APPLICANT: Rufos, Roger
; TITLE OF INVENTION: Peptide-sensitive modified Bacillus thuringiensis insecticidal
; FILE REFERENCE: A35992-PCT-USA-A (072667.0191)
; CURRENT APPLICATION NUMBER: US/10/665,460A
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/FR02/00772
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR 01/03691
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence description: Cry9cal Glu-164
; NAME/KEY: CDS
; LOCATION: (1)..(2019)
US-10-665-460A-7

Query Match 5.6%; Score 113.4; DB 7; Length 2019;
Best Local Similarity 55.8%; Pred. No. 7e-16;
Matches 294; Conservative 0; Mismatches 206; Indels 27; Gaps 3;

QY 401 ATTATATCTTCAATATCTTGAAGATTGGCTTACAGATTAATCAATCTTAATAAATCTTG 460
Db 440 ATGTATATCAAGCTTCCCTTCAAAATTTGGTGTGATGAAATGATACGAGAAATTTAA 499
QY 461 CTGACGTAGTTAAACGTTCCAGACCGGAGAGAAATTTCACTAACTTTAGCGGGT 520
Db 500 GTGTTGTGCTGCTCAATTAATTAATGACCTTAATTTGTTAATGCTATTCGA---T 556
QY 521 CATTATCAAGACAGAAAGCTGAATTTATTTATTTGCTAGTATGCAAGCTGCAAAATG 580
Db 557 TGTTCAGATTAATGACACGACGATTCATTAAGTATGATGATGACAGAGTGTGAAT 616
QY 581 TGCATTTATCTATTAAGGAGCAGATTAATATTAATAAAGAAATGGGACATGATGTGTC 640
Db 617 TACATTTGTTATTAATTAAGAAATGATGATCTTTTGGAGAGAGATGGGATTCG----- 670
QY 641 CACCGTTGATCCAGGTCAGGAGAACTGATTTGAACGAGCGGTTAAAGGCAAAATTA 700
Db 671 -----CACAGGGGAAATTTCACATTAATTAAGCCTCAATTTGGAATTAACCG 718
QY 701 AAGAGTATCTAATTTATGTTAGGTTGATTAACAAGGTTTATGATGATGATGACAGG 760
Db 719 CTAGATACACTAATTAATGATGAACCTGATTAATACAGGTTTATGATGATTAAG----- 774

Qy	761	CGGGTACAGTGTGGAAGTTGGTCGAAATTTAATAAATTTGCTAGAGAAATGACGTTGG	820
Db	775	--GGAACAAATACTGAAAGTTGGTTAAGATATCATCATTCGTAAGAAATGACTTTAG	832
Qy	821	CGGTATTTGATATTAATTTGCTAATATTTCCAACTTATGATTTTGAAAAATATCCATTAGCAA	880
Db	833	TGGTATTAGATGTTGGCGCTATTTCCATATTATGATGTAAGCACTTTATCCAAAGGGAT	892
Qy	881	CAAGGTAGAGTTAACTAGGAAATTTATACAGATCCAGTGGATAT	927
Db	893	CAAAACCACAGCTTACACGTGAGTATATACAGATCCGATTTGTATTT	939

Search completed: December 19, 2005, 13:41:22
 Job time : 1105.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:54:29 ; Search time 189.099 Seconds
(Without alignments)
5233.604 Million cell updates/sec

Title: US-10-782-141-2

Perfect score: 2019
Sequence: 1 gggaaaaaatgaattctta.....atagttatattcaattaa 2019

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCF_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
9: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	5.2	1860	7 US-11-058-727-15	Sequence 15, Appl
2	105	5.2	1860	7 US-11-108-389-15	Sequence 15, Appl
3	105	5.2	2010	7 US-11-058-727-11	Sequence 11, Appl
4	105	5.2	2010	7 US-11-108-389-11	Sequence 11, Appl
5	105	5.2	3621	7 US-11-058-727-1	Sequence 1, Appl
6	105	5.2	3621	7 US-11-108-389-1	Sequence 1, Appl
7	105	5.2	4874	7 US-11-058-727-17	Sequence 17, Appl
8	105	5.2	4874	7 US-11-108-389-17	Sequence 17, Appl
9	101.8	5.0	2019	7 US-11-058-727-87	Sequence 87, Appl
10	101.8	5.0	2019	7 US-11-058-727-87	Sequence 87, Appl
11	101.8	5.0	2019	7 US-11-108-389-55	Sequence 55, Appl
12	101.8	5.0	2019	7 US-11-108-389-87	Sequence 87, Appl
13	100.2	5.0	2019	7 US-11-058-727-59	Sequence 59, Appl
14	100.2	5.0	2019	7 US-11-058-727-91	Sequence 91, Appl
15	100.2	5.0	2019	7 US-11-108-389-59	Sequence 59, Appl
16	100.2	5.0	2019	7 US-11-108-389-91	Sequence 91, Appl
17	99.4	4.9	4359	9 US-11-031-643-3	Sequence 3, Appl
18	98.6	4.9	1863	7 US-11-058-727-19	Sequence 19, Appl
19	98.6	4.9	1863	7 US-11-108-389-19	Sequence 19, Appl
20	98.6	4.9	2019	7 US-11-058-727-57	Sequence 57, Appl
21	98.6	4.9	2019	7 US-11-058-727-89	Sequence 89, Appl
22	98.6	4.9	2019	7 US-11-108-389-57	Sequence 57, Appl
23	98.6	4.9	2019	7 US-11-108-389-89	Sequence 89, Appl

24	98.6	4.9	2022	7 US-11-058-727-7	Sequence 7, Appl
25	98.6	4.9	2022	7 US-11-058-727-21	Sequence 21, Appl
26	98.6	4.9	2022	7 US-11-058-727-25	Sequence 25, Appl
27	98.6	4.9	2022	7 US-11-058-727-29	Sequence 29, Appl
28	98.6	4.9	2022	7 US-11-058-727-33	Sequence 33, Appl
29	98.6	4.9	2022	7 US-11-058-727-43	Sequence 43, Appl
30	98.6	4.9	2022	7 US-11-058-727-49	Sequence 49, Appl
31	98.6	4.9	2022	7 US-11-058-727-67	Sequence 67, Appl
32	98.6	4.9	2022	7 US-11-058-727-69	Sequence 69, Appl
33	98.6	4.9	2022	7 US-11-058-727-75	Sequence 75, Appl
34	98.6	4.9	2022	7 US-11-058-727-81	Sequence 81, Appl
35	98.6	4.9	2022	7 US-11-108-389-7	Sequence 7, Appl
36	98.6	4.9	2022	7 US-11-108-389-21	Sequence 21, Appl
37	98.6	4.9	2022	7 US-11-108-389-25	Sequence 25, Appl
38	98.6	4.9	2022	7 US-11-108-389-29	Sequence 29, Appl
39	98.6	4.9	2022	7 US-11-108-389-33	Sequence 33, Appl
40	98.6	4.9	2022	7 US-11-108-389-43	Sequence 43, Appl
41	98.6	4.9	2022	7 US-11-108-389-49	Sequence 49, Appl
42	98.6	4.9	2022	7 US-11-108-389-67	Sequence 67, Appl
43	98.6	4.9	2022	7 US-11-108-389-69	Sequence 69, Appl
44	98.6	4.9	2022	7 US-11-108-389-75	Sequence 75, Appl
45	98.6	4.9	2022	7 US-11-108-389-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-11-058-727-15
Sequence 15, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Quo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: 49PVD
US-11-058-727-15
Query Match 5.2%, Score 105, DB 7, Length 1860;
Best Local Similarity 53.1%, Pred. No. 4.5e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;
CY GCACTTCATATGATGATTTATGATCTATATTCGTAAGAGGTAGACGAGCGGTGA 354


```
Db 205 GAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATATAGCAATATGCAAG 264
QY 355 AGTGAAGGGGTTCACATTTTGGGGTGAATGACGCTTATCAAGTATATCTTCAT 414
Db 265 AATTAAGCGCTTTCGGAATTTAGAGATTAGTAAATTAATTCAGAA---TTATATCTTACT 321
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAAAACTTGCTGAGTATTA 474
Db 322 GGGCTTGAAGATGGAAGAAATCCAAATGTTCAAGACCTTAGAGATGTGCAGAAAT 381
QY 475 CAGTCCAAAGCAGGGAAGAAATTCCTAACTTTTACAGAGGTCATATTCAGACAG 534
Db 382 CGATTTGAATCTCGATAGTTATTTATCCCAATATATGCCA---TCTTTAGAGTAC 438
QY 535 AAAGCTGAATATATATTCCTAGTATGTCAGCAAGCTGCAATGTGATTTATCTACT 594
Db 439 AATTTTGAAGTACATTCCTTACTGTATGCAATGCGACCACTTCACTTTTACTGTTA 498
QY 595 TTAAGGAGCGCAGTTAAATTAATAAAGAAATGGGGACTAGTGTGTCACCGTTGTATCCA 654
Db 499 TTTAAGGAGCGCGTCATTTTTTGGAGAAGAAATGGGGA-----TGTGCA 540
QY 655 GGGTCAGGGAACCTGATTTGTAACGACGGTTAAAAAGCAAAATAAAGATATCTAAT 714
Db 541 ACAACTACTATATTAATTAATTAATGATCGTCAATGAACTTACTGAGATATTTCTGAT 600
QY 715 TATGTGTAGGGGTGATTAACAAGGGTTTATGATCAGATTAAGACGGGTCATCAAGTGT 774
Db 601 CACTGTGTAAAGTGTATGAACTGTTTATGCAAAATTTAAA-----GGCAGACGGCT 654
QY 775 GAAGTTTGTGCAAAATTTTAATAATTTTCTAGAGAAATGACGTTGGCGGTATGATAT 834
Db 655 AAAAATGGGTGACATTAACAATTCGTTAGAGAAATGACACTGGGGTTTATGATGTT 714
QY 835 ATTGCTATATTTTCAACTTATGATTTTGGAAAAATATCCATTAGCAACAGTGTAGT 894
Db 715 GTTGCAATTAATCCCAATTAATGACACGCACTACCAATGAAAGCAACACTA 774
QY 895 ACTAGGGAATTTTATACAGATCCAGTGGG 923
Db 775 ACAAGGAAGTATATACAGATCCACTGGG 803

RESULT 2
US-11-108-389-15
; Sequence 15, Application US/11108389
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
```

```
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) ... (1860)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15

Query Match 5.2%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 4.5e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACCTTCTATATGATTTAGTATCTATTAATTCGTAAGAGTAGACAGACGCTGTA 354
Db 205 GAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATATAGCAATATGCAAG 264
QY 355 AGTGAAGGGGTTCACATTTTGGGGTGAATGACGCTTATCAAGTATATCTTCAT 414
Db 265 AATTAAGCGCTTTCGGAATTTAGAGATTAGTAAATTAATTCAGAA---TTATATCTTACT 321
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAAAACTTGCTGAGTATTA 474
Db 322 GGGCTTGAAGATGGAAGAAATCCAAATGTTCAAGACCTTAGAGATGTGCAGAAAT 381
QY 475 CAGTCCAAAGCAGGGAAGAAATTCCTAACTTTTACAGAGGTCATATTCAGACAG 534
Db 382 CGATTTGAATCTCGATAGTTATTTATCCCAATATATGCCA---TCTTTAGAGTAC 438
QY 535 AAAGCTGAATATATATTCCTAGTATGTCAGCAAGCTGCAATGTGATTTATCTACT 594
Db 439 AATTTTGAAGTACATTCCTTACTGTATGCAATGCGACCACTTCACTTTTACTGTTA 498
QY 595 TTAAGGAGCGCAGTTAAATTAATAAAGAAATGGGGACTAGTGTGTCACCGTTGTATCCA 654
Db 499 TTTAAGGAGCGCGTCATTTTTTGGAGAAGAAATGGGGA-----TGTGCA 540
QY 655 GGGTCAGGGAACCTGATTTGTAACGACGGTTAAAAAGCAAAATAAAGATATCTAAT 714
Db 541 ACAACTACTATTAATTAATTAATGATCGTCAATGAACTTACTGAGATATTTCTGAT 600
QY 715 TATGTGTAGGGGTGATTAACAAGGGTTTATGATCAGATTAAGACGGGTCATCAAGTGT 774
Db 601 CACTGTGTAAAGTGTATGAACTGTTTATGCAAAATTTAAA-----GGCAGACGGCT 654
QY 775 GAAGTTTGTGCAAAATTTTAATAATTTTCTAGAGAAATGACGTTGGCGGTATGATAT 834
Db 655 AAAAATGGGTGACATTAACAATTCGTTAGAGAAATGACACTGGGGTTTATGATGTT 714
QY 835 ATTGCTATATTTTCAACTTATGATTTTGGAAAAATATCCATTAGCAACAGTGTAGT 894
Db 715 GTTGCAATTAATCCCAATTAATGACACGCACTACCAATGAAAGCAACACTA 774
QY 895 ACTAGGGAATTTTATACAGATCCAGTGGG 923
Db 775 ACAAGGAAGTATATACAGATCCACTGGG 803

RESULT 3
US-11-058-727-11
; Sequence 11, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
```

```

; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-058-727-11

Query Match      5.2%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 4.7e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTTCTATATGATTTAGTATCTATATTCGTAAGAGGTAGACGAGCGTGTTA 354
DB 337 GAATTTTATGGAACAAGTAAAGAACTCATATATCAAAAATGAGAGATATGCAAG 396
QY 355 AGTACGGGGTTCAGATTTTGGAGGTAATGACGCTGATCAAGATATATCTTCAT 414
DB 397 AATTAAGCGCTTTCGAAATTAAGAGATTAGTATATATATCAAA--TTATATCTACT 453
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAACCTTGCTGACGTATTA 474
DB 454 GCGCTTGAAGATGGGAAGAAATCCAAATGCTTCAAGAGCTTACAGAGATGCGAAT 513
QY 475 CAGTTCACAGACGGGAGAGAGATTTCATTAACCTTTAGCAGGTCATATCAAGAC 534
DB 514 CGATTTGAATCCGATAGTATTTATTCGCAATATATGCCA--TCCTTTAGAGTACA 570
QY 535 AAAGCTGAATATATATATGCTACGATATGCAAGTGCATATGCAATTTATCTA 594
DB 571 AATTTTGAAGTACCATTCCTTACTGTATATGCAATGCGACCAACCTTCATTTACTGTTA 630
QY 595 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGAGCTAGTGTGCCACGTTGTATCA 654
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 672
QY 655 GGGTCAGGAGCACTGATTTGTAACGACGGTTAAAGCGAAATTAAGAGTATCTAAT 714
DB 673 ACAACTACTATTAATCTATATTAATGATCGTCAAACTGAACTTACGAGAAATTTCTGAT 722
QY 715 TATTTGTAGGGTGTATTAACAAGGGTTAGATCAGATTAAGACAGGGGGTATCAAGTCT 774
DB 733 CACTGTATTAAGGTATGAACTGCTTTAGCAAAATTAATA-----GGCAGCAGGCT 786
QY 775 GAAGTTGTGCGAATTTAATAAATTTCTAGAGAAATGACGTTGGCGGTATGGAATTT 834
DB 787 AAACAAGGGGTGCTATTAACAATTCGATAGAGAAATGACACTGGGGTTTATGATGTT 846
QY 835 ATTTGCTATTTTCAACTTATGATTTTGAAGAAATATCATTAAGCAAGAATGATGATTA 894
DB 847 GTTGCATTTATTTCCAAATTAATGACACACGACGTAACCAATGGAAGCAAGCAACTA 906
QY 895 ACTAGGGAATTTATACAGATCCAGTGGG 923
DB 907 ACAAGGGAAGTATATACAGATCCACTGGG 935
```

```

RESULT 4
US-11-108-389-11
; Sequence 11, Application US/11108389
; Publication No. US20050261188A1.
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-108-389-11

Query Match      5.2%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 4.7e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTTCTATATGATTTAGTATCTATATTCGTAAGAGGTAGACGAGCGTGTTA 354
DB 337 GAATTTTATGGAACAAGTAAAGAACTCATATATCAAAAATGAGAGATATGCAAG 396
QY 355 AGTACGGGGTTCAGATTTTGGAGGTAATGACGCTGATCAAGATATATCTTCAT 414
DB 397 AATTAAGCGCTTTCGAAATTAAGAGATTAGTATATATATCAAA--TTATATCTACT 453
QY 415 TATCTTGAGATTGGCTTACAGATTAATCAATCTTAAACCTTGCTGACGTATTA 474
DB 454 GCGCTTGAAGATGGGAAGAAATTCCAATGCTTCAAGAGCTTACAGAGATGCGAAT 513
QY 475 CAGTTCACAGACGGGAGAGAGATTTCATTAACCTTTAGCAGGTCATATCAAGAC 534
DB 514 CGATTTGAATCCGATAGTATTTATTCGCAATATATGCCA--TCCTTTAGAGTACA 570
QY 535 AAAGCTGAATATATATATGCTACGATATGCAAGTGCATATGCAATTTATCTA 594
DB 571 AATTTTGAAGTACCATTCCTTACTGTATATGCAATGCGACCAACCTTCATTTACTGTTA 630
QY 595 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGAGCTAGTGTGCCACGTTGTATCA 654
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 672
QY 655 GGGTCAGGAGCACTGATTTGTAACGAGCGTTAAAGCGAAATTAAGAGTATCTAAT 714
DB 673 ACAACTACTATTAATCTATATTAATGATCGTCAAACTGAACTTACGAGAAATTTCTGAT 722
```

QY	475	CAGTTCGAAGCAGCGGAGAGAGATTCTCTAAACTTTTATGACGGGTCAATTATCAAGACAG	5344
Db	514	CGATTTGGAATCCTGGATAGTTTATTTACGGAATATATGCCA---TCCTTTAGAGTGACA	5700
QY	535	AAAGCTGAATAATNTATATTTATGCTCTACGATGATGCAAGCTGGAANTGCAATTTATCTA	5944
Db	571	AAATTTGAAGTACATTCTTACTATATATGCAATGGCAGCAACTTCAATTAATGTTA	6300
QY	595	TTAAGGACGCAAGTTTAAATATATAAAAAAGATGGGACATGATGTGTCCACCGTTGTATCCA	6544
Db	631	TTTAAAGGACGCGTCAATTTTGTGAGAGAAATGGGGA-----TGGTCA	6722
QY	655	GGGTCAAGGAGAACTGATTTGTACGACGCGGTTTAAAGCGAAATATAAGATATCTAAT	7144
Db	673	ACAACCTACTAT	7322
QY	715	TATTTGTATGGGAGGTATATCAAGGGTTTATGATCAGATATACAGACGGCGGTATCAAGTCT	7744
Db	733	CACGTGTATAAAGTGTATATAAACTGTTTATGCAAAATTTAAA-----GGCAGACGGCT	7866
QY	775	GAAAGTTTGTGCAATTTAT	8344
Db	787	AAACAATGGGTGTGACTATATACCAATTCGTTAGAGAAATGACATGGCGGTTTATGATGT	8466
QY	835	ATTGCTATATTTTCCAACTATATATTTTGAATAAAATATTCATTATAGCAACAGTATAGTTA	8944
Db	847	GTTGCATTTATTTCCCAATATATATACACACGACGATCCCAATGAGAAAGCAACACTA	9066
QY	895	ACTAGGAAATTTATATACATCCAGTGGG	923
Db	907	ACAAGGAAATATATACATCCAGTGGG	935
RESULT 6			
US-11-108-389-1			
Sequence 1, Application US/11108389			
Publication No. US20050261188A1			
GENERAL INFORMATION:			
APPLICANT: Andre R. Abad			
APPLICANT: Ronald D. Flannagan			
APPLICANT: Rafael Herrmann			
APPLICANT: Theodore W. Kahn			
APPLICANT: Albert L. Lu			
APPLICANT: Billy Fred McCutchen			
APPLICANT: James K. Presnail			
APPLICANT: James F.H. Wong			
APPLICANT: Cao-Guo Yu			
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal			
TITLE OF INVENTION: Activity			
FILE REFERENCE: 35718/291049			
CURRENT APPLICATION NUMBER: US/11/108,389			
CURRENT FILING DATE: 2005-04-18			
PRIOR APPLICATION NUMBER: 60/391,786			
PRIOR FILING DATE: 2002-06-26			
PRIOR APPLICATION NUMBER: 60/460,787			
PRIOR FILING DATE: 2003-04-04			
PRIOR APPLICATION NUMBER: 10/606,320			
PRIOR FILING DATE: 2003-06-25			
NUMBER OF SEQ ID NOS: 134			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 1			
LENGTH: 3621			
TYPE: DNA			
ORGANISM: Bacillus thuringiensis			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)...(3621)			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (0)...(0)			
OTHER INFORMATION: Cry12I8-1			
US-11-108-389-1			

Query Match 5.2%; Score 105; DB 7; Length 3621;
Best Local Similarity 53.1%; Pred. No. 6e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTCTATATGATTTAGTATCTATATTTGTTAAAGAGTAGACGAGCGTGTGA 354
DB 337 GAAATTTTATGCAACAGTAGAAGAACTCATTAATCAAAAAGAGATATGCAAG 396
QY 355 AGTACGGGGTTCAGATTTTGAAGGTGAATGACTCTTATCAAGATTAATCTTCAT 414
DB 397 AATTAAGCGCTTCGGAATTAAGAGATGATGATATTAATCAAA--TTATATCTACT 453
QY 415 TATCTTGAAGATGCGCTTACAGATAATCAATCTTAAAAAATCTGCTGAGTAGTAA 474
DB 454 GCGCTTAAAGAAATGGGAAGAAATCCAAATGTTCAAGAGCTTACAGAGATGTCGAAT 513
QY 475 CAGTTCCAGACGAGGAAGAGATTTCACTTAACTTTAGAGGCTGATTAACAAG 534
DB 514 CGATTTGAAATCTGGATAGTTATTTACGCAATATATGCCA--TCTTTAGAGTACA 570
QY 535 AAAGCTGAATATTTATTTATGCTTACGTATGCAAGCTGCAATGCAATTTATTA 594
DB 571 AATTTGAAGTACCATTCCTTACGTATATGCAATGCAAGCAACTTCTTATCTGTA 630
QY 595 TTAAGGACGCGATTAATATTAATAAAGATGGGAGCTAGTGTGTCACCGTGTATCA 654
DB 631 TTAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 672
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGATATCTAAT 714
DB 673 ACAACTACTATTAATATCTATATATGATGTCAAATGAACTTATGCAAGATATTCAT 732
QY 715 TATTTGTAGGGTGTGTAACAAGGTTTAGATCAGATTAAGACAGCGGGTACAAAGTCT 774
DB 733 CACTGTATAAGTGTATGAAACGTTTACCAAAATTTAAA-----GGCAGAGCGCT 786
QY 775 GAAGTTTGTGCAATTAATTAATTTCTGTAAGAAATGACGTTGGCGGTATGATAT 834
DB 787 AAACAATGGGTGACTATTAACCAATTCGTATAGAAATGACACTGGGGTTTATGATGT 846
QY 835 ATTGCTATTTTCCAACTTATGATTTGAAAAATATCATTAAGCAACAGTATGATTA 894
DB 847 GTTGCAATATTTCCAAATTTATGACACAGCAGTACCAATGAAAGCAACACTA 906
QY 895 ACTAGGAAATTTATACAGATCCAGTGG 923
DB 907 ACAAGGAGATATATACAGATCCAGTGG 935

RESULT 7
US-11-058-727-17
; Sequence 17, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prensail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058.727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-058-727-17

Query Match 5.2%; Score 105; DB 7; Length 4874;
Best Local Similarity 53.1%; Pred. No. 6.8e-16;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 295 GCACTTCTATATGATTTAGTATCTATATTTGTTAAAGAGTAGACGAGCGTGTGA 354
DB 1067 GAAATTTTATGCAACAGTAGAAGAACTCATTAATCAAAAATGACAGATATGCAAG 1126
QY 355 AGTACGGGGTTCAGATTTTGAAGGTGAATGACTCTTATCAAGATTAATCTTCAT 414
DB 1127 AATTAAGCGCTTCGGAATTAAGAGATGATGATATTAATCAAA--TTATATCTACT 1183
QY 415 TATCTTGAAGATGCGCTTACAGATAATCAATCTTAAAAAATCTGCTGAGTAGTAA 474
DB 1184 GCGCTTGAAGAAATGGGAAGAAATCCAAATGTTCAAGAGCTTACAGAGATGTCGAAT 1243
QY 475 CAGTTCCAGACGAGGAAGAGATTTCACTTAACTTTAGAGGCTGATTAACAAG 534
DB 1244 CGATTTGAAATCTGGATAGTTATTTACGCAATATATGCCA--TCTTTAGAGTACA 1300
QY 535 AAAGCTGAATATTTATTTATGCTTACGTATGCAAGCTGCAATGCAATTTATTA 594
DB 1301 AATTTGAAGTACCATTCCTTACGTATATGCAATGCAAGCAGCAACTTATTA 1360
QY 595 TTAAGGACGCGATTAATATTAATAAAGATGGGAGCTAGTGTGTCACCGTGTATCA 654
DB 1361 TTAAGGACGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 1402
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAACGAAATTAAGATATCTAAT 714
DB 1403 ACAACTACTATTAATATCTATATATGATGTCAAATGAACTTATGCAAGATATTCAT 1462
QY 715 TATTTGTAGGGTGTGTAACAAGGTTTAGATCAGATTAAGACAGCGGGTACAAAGTCT 774
DB 1463 CACTGTATAAGTGTATGAAACGTTTACCAAAATTTAAA-----GGCAGAGCGCT 1516
QY 775 GAAGTTTGTGCAATTAATTAATTTCTGTAAGAAATGACGTTGGCGGTATGATTA 834
DB 1517 AAACAATGGGTGACTATTAACCAATTCGTATAGAAATGACACTGGCGGTTTATGATGT 1576
QY 835 ATTGCTATTTTCCAACTTATGATTTGAAAAATATCATTAAGCAACAGTATGATTA 894
DB 1577 GTTGCAATATTTCCAAATTTATGACACAGCAGTACCAATGAAAGCAACACTA 1536
QY 895 ACTAGGAAATTTATACAGATCCAGTGG 923
DB 1637 ACAAGGAGATATATACAGATCCAGTGG 1665

RESULT 8
US-11-108-389-17
; Sequence 17, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu

```
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4874
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17
```

Query Match 5.2%; Score 105; DB 7; Length 4874;

Best Local Similarity 53.1%; Pred. No. 6,8e-16; Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

```
295 GCACCTTCTATATGATATTAGTATCTATATATCGTAAAGAGTACGAGACGCTGTTA 354
1067 GAATTTTATGGAACAAGAGAGAACTCATTTATCAAAAATAGCAAAATATGCAAG 1126
355 AGTACGGGGTTCAGATTTTGAAGGTGAATGACTGCTTATCAAGATTAATCTTCAT 414
1127 AATAAAGCGCTTCGGAATTAGAAGATAGTAATATTAATTAACAA--TTATATCTAAGT 1183
415 TATCTTGAGATGCTGCTACAGATTAATCAATCCCTTAATAAACTTGCTGACGTATTA 474
1184 GCGCTTGAAGAAAGGAGAGAAATCCAAATGCTTCAAGACCTTAAGAGTGTGCGAAAT 1243
475 CAGTTCAGACGAGGAGAAAGATTCACCTAACTTTAGCAGAGTCAATATCAAGACAG 534
1244 CAGTTTGAATCCTGATAGTTATTTAGCAATATATGCA--TCTTTAGAGTGAC 1300
535 AAAGTGAATATTTATTTATGCTTACGTATGTGCAAGCTGCAATGTGCAATTTTACTA 594
1301 AATTTTGAAGTACATTTCTTACTGTATATGCAATGCGACGCAACCTTCACTTACTGTTA 1360
595 TTAAGGAGCGCATTTAATTAATAAAGAAATGGGAGTATGTGTCCACCGTTGTATCA 654
1361 TTAAGGAGCGCATTTTGTGAGAGAAATGGGGA-----TGGTCA 1402
655 GGGTCAAGGAGACATGATTTGTAAGAGCGGTAAAGCGAAATTAAGATTAATTAAT 714
1403 ACACTACTATTAATTAATCTTTATGATCGTCAAAATGAACCTTCTGCAATATTTCTGAT 1462
715 TATTTGTAGGAGGTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGGTATCAAGTGT 774
1463 CACTGTGTAAAGTGTATGAAACGTGGTTAGCAAAATTTAAA-----GGCAGACGGCT 1516
775 GAAGTTTGTGCAAAATTTAATAATTTCTGATGAAGAAATGACGTTGGCGGTATTTGATAT 834
1517 AAACAATGGGTGATCAATTAACAATTTCCGTAGGAATATGACATGCGGGGTTTATGATGTT 1576
835 ATTGCTATATTTCCAACTTATGATTTTGAATAATATCCATTAGCAACAAGTGTAGATTA 894
1577 GTTGCAATATTTCCAAATTTATGACACGACGATCCCAATGAGAAAGCAACAATA 1636
895 ACTAGGAAATTTATACAGATCCAGTGGG 923
```

Db 1637 ACAAGGAAATATATACAGATCCAGTGGG 1665

RESULT 9

US-11-058-727-55

Sequence 55, Application US/11058727

Publication No. US20050261483A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Albert L. Lu

APPLICANT: Billy Fred McCutchen

APPLICANT: James K. Presnall

APPLICANT: James F. H. Wong

APPLICANT: Cao-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal

FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: US/11/058,727

PRIOR FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/391,786

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 55

LENGTH: 2019

TYPE: DNA

ORGANISM: Bacillus thuringiensis (mutated)

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(2019)

US-11-058-727-55

Query Match 5.0%; Score 101.8; DB 7; Length 2019;

Best Local Similarity 58.6%; Pred. No. 2.8e-15;

Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
535 AAAGTGAATATTTATTTATGCTTACGTATGCAAGCGCAAAATGATTAATTAATCA 594
583 AATTTTGAAGTACATTTCTTACTGTATATGCAATGCGACCACTTCACTTACTGTTA 642
595 TTAAGGAGCGCATTTAATTAATAAAGAAATGGGAGTATGTGTCCACCGTTGTATCA 654
643 TTAAGGAGCGCATTTTGTGAGAGAAATGGGGA-----TGGTCA 684
655 GGGTCAAGGAGACATGATTTGTAAGAGCGGTAAAGCGAAATTAAGATTAATTAAT 714
685 ACACTACTATTAATTAATCAATTTATGATCGTCAAAATGAAACCTTACGCAATATTTCTGAT 744
715 TATTTGTAGGAGGTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGGTATTAAT 774
745 CACTGTGTAAAGTGTATGAAACGTGGTTAGCAAAATTTAAA-----GGCAGACGGCT 798
775 GAAGTTTGTGCAAAATTTAATAATTTCTGATGAAGAAATGACGTTGGCGGTATTTGATAT 834
799 AAACAATGGGTGATCAATTAACAATTTCCGTAGGAATATGACATGCGGGGTTTATGATGTT 858
859 GTTGCAATATTTCCAAATTTATGACACGACGATCCCAATGAGAAAGCAACAATA 918
895 ACTAGGAAATTTATACAGATCCAGTGGG 923
919 ACAAGGAAATTTATACAGATCCAGTGGG 947
```

RESULT 10

US-11-058-727-87
; Sequence 87, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis* (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-87

Query Match 5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2.8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
QY 535 AAAGCTGAATATATTATTATGCTACGATGTCGCAAGCTGCAAAATGTCATTATCTA 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AATTTGAAGTACATTCCTTACTGATATGCAATGCGCAACCTTCTTACTGTTA 642
QY 595 TTAAAGGAGCGCACTTAAATATATAAAGAAATGGGACTAGTGTCTCCACCGTTGTATCA 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TTAAAGGAGCGCACTTAAATATATAAAGAAATGGGACTAGTGTCTCCACCGTTGTATCA 684
QY 655 GGGTCAGGAGAACTGATTTGTACGAGCGGTTAAACGAAATATAAGATATCTAAT 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 ACAACTACTATTTAATACTATTATGATCGTCAAACTTACTGCAAAATATCTGAT 744
QY 715 TATTTGTAGGGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGGTACAAAGTCT 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CACTGTATAAGTGTATGAACTGTTTAGCAAAATTTAAA-----GGCAGAGCGCT 788
QY 775 GAAGTTTGTGCAATTTAATAAATTTGTAAGAAATGACGTTGGCGGTATTTGATAT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACATGGGCGTTTATGATGTT 858
QY 835 ATTGCTATATTTCCAACTTATGATTTGAAAATATATCATTAGCAACAAGTGTAGATTA 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTTGCAATTATTTCCCAATTTATGACAAATACGTAACGTAACCAATAGAAAGCAACAATA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947
```

RESULT 11
US-11-108-389-55
; Sequence 55, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:

APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 2019
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-11-108-389-55

Query Match 5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2.8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
QY 535 AAAGCTGAATATATTATTATGCTACGATGTCGCAAGCTGCAAAATGTCATTATCTA 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AATTTGAAGTACATTCCTTACTGATATGCAATGCGCAACCTTCTTACTGTTA 642
QY 595 TTAAAGGAGCGCACTTAAATATATAAAGAAATGGGACTAGTGTCTCCACCGTTGTATCA 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TTAAAGGAGCGCACTTAAATATATAAAGAAATGGGACTAGTGTCTCCACCGTTGTATCA 684
QY 655 GGGTCAGGAGAACTGATTTGTACGAGCGGTTAAACGAAATATAAGATATCTAAT 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 ACAACTACTATTTAATACTATTATGATCGTCAAACTTACTGCAAAATATCTGAT 744
QY 715 TATTTGTAGGGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGGTACAAAGTCT 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 CACTGTATAAGTGTATGAACTGTTTAGCAAAATTTAAA-----GGCAGAGCGCT 788
QY 775 GAAGTTTGTGCAATTTAATAAATTTGTAAGAAATGACGTTGGCGGTATTTGATAT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACATGGGCGTTTATGATGTT 858
QY 835 ATTGCTATATTTCCAACTTATGATTTGAAAATATATCATTAGCAACAAGTGTAGATTA 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTTGCAATTATTTCCCAATTTATGACAAATACGTAACGTAACCAATAGAAAGCAACAATA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947
```

RESULT 12
US-11-108-389-87
; Sequence 87, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn

```

; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-108-389-87
```

```

Query Match          5.0%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 2,8e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;
```

```

QY 535 AAAGCTGAATATATATATATGCTAGTATGTCAGTCAAGTGCAGAAATGCAATTATTACTA 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 583 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCACTTCAATTACTGTTA 642
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 595 TTAAGGAGCGAGTAAATATATATATATATATATATATATATATATATATATATATAT 654
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAGAAATGGGA-----TGCTCA 684
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATATTAAT 714
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 685 ACAACTACTATATATATATATATATATATATATATATATATATATATATATATATAT 744
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 715 TATGTGTAGGGGTGATATACAGGGTTAGATCAGATTAAGACGGGGTAAAGTGTCT 774
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 745 CACTGTGTAAAGTGTATGAACTGGTTTACAAATTTAAA-----GGCAGAGCGCT 798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 GAAGTTGTGCAATTTATATATATATATATATATATATATATATATATATATATATAT 834
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AAACATGGGTGATATATATATATATATATATATATATATATATATATATATATATAT 858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 ATTGCTATATTTTCAACTTATATATATATATATATATATATATATATATATATATATAT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GTTGCAATTTTCCCAATTTATATATATATATATATATATATATATATATATATATATAT 918
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 ACTAGGAAATTTATATATATATATATATATATATATATATATATATATATATATATAT 923
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 ACAAGGAAATTTATATATATATATATATATATATATATATATATATATATATATATAT 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 13
US-11-058-727-59
; Sequence 59, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
```

```

; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-59
```

```

Query Match          5.0%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 6,8e-15;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;
```

```

QY 535 AAAGCTGAATATATATATATGCTAGTATGTCAGTCAAGTGCAGAAATGCAATTATTACTA 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 583 AATTTTGAAGTACCATTTCTTACTGTATATGCAATGCGACCACTTCAATTACTGTTA 642
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 595 TTAAGGAGCGAGTAAATATATATATATATATATATATATATATATATATATATATATAT 654
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 643 TTAAGGAGCGGTCATTTTGGAGAGAAATGGGA-----TGCTCA 684
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 655 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATATTAAT 714
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 685 ACAACTACTATATATATATATATATATATATATATATATATATATATATATATATAT 744
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 715 TATGTGTAGGGGTGATATACAGGGTTAGATCAGATTAAGACGGCGGTTATCAAGTGTCT 774
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 745 CACTGTGTAAAGTGTATGAACTGGTTTACAAATTTAAA-----GGCAGAGCGCT 798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 GAAGTTGTGCAATTTATATATATATATATATATATATATATATATATATATATATATAT 834
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 AAACATGGGTGATATATATATATATATATATATATATATATATATATATATATATATAT 858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 ATTGCTATATTTTCAACTTATATATATATATATATATATATATATATATATATATATATAT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 GTTGCAATTTTCCCAATTTATATATATATATATATATATATATATATATATATATATATAT 918
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 ACTAGGAAATTTATATATATATATATATATATATATATATATATATATATATATATATAT 923
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 ACAAGGAAATTTATATATATATATATATATATATATATATATATATATATATATATATAT 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 14
US-11-058-727-91
; Sequence 91, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: Cao-Guo Yu
; APPLICANT: James F.H. Wong
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
```



```

; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-91

```

```

Query Match
Best Local Similarity 5.0%; Score 100.2; DB 7; Length 2019;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;

```

```

QY 535 AAAGCTGAATATTTATTTATGCTTACGATATGTCAGCACTGCAATGTCATTATTTACTA 594
DB 583 AATTTGAAGTACCATTCCTTACTGATATGCAATGCGACCAACTTCACTTTACTGTTA 642
QY 595 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGACTAGTGTCTCCACGGTGTATCCA 654
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 655 GGGTCAGGAGAACTGATTTGTAAGAGCGGTTAAACGAAATTAAGAATTAATTTACTAAT 714
DB 685 ACAACTACTATTTATTAATCTATTTATGATGTCGCAATGAACTTCTGCAAGATTTTCAT 744
QY 715 TATTGTGAGGCTGTATTAACAAGGTTTATGATCAATAAGACAGCGGGTACAGTGTCT 774
DB 745 CACTGTGTAAGTGTATGAACTGCTTTAGCAAAATTAATA-----GGCAGAGCGCT 798
QY 775 GAAGTTGTGCGAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 834
DB 799 AAACATGAGGTGATCTATTAACCAATTCCTGAGAAATGACACTGGCGGTTTATGATGTT 858
QY 835 ATTGCTATATTTTCAACTTATGATTTTGAATAATATCCATTAGCAACAGTGTATGATTA 894
DB 859 GTTGCAATTATTTCCCAATTAATGACAAATACGTAACCAATGGAATGAAAGACAACTA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
DB 919 ACAAGGAAATATATACAGATCCAGTGGG 947

```

RESULT 15

```

US-11-108-389-59
; Sequence 59, Application US/11/108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26

```

```

; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-108-389-59

```

```

Query Match
Best Local Similarity 5.0%; Score 100.2; DB 7; Length 2019;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;

```

```

QY 535 AAAGCTGAATATTTATTTATGCTTACGATATGTCAGCACTGCAATGTCATTATTTACTA 594
DB 583 AATTTGAAGTACCATTCCTTACTGATATGCAATGCGACCAACTTCACTTTACTGTTA 642
QY 595 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGACTAGTGTCTCCACGGTGTATCCA 654
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 655 GGGTCAGGAGAACTGATTTGTAAGAGCGGTTAAACGAAATTAAGAATTAATTTACTAAT 714
DB 685 ACAACTACTATTTATTAATCTATTTATGATGTCGCAATGAACTTCTGCAAGATTTTCAT 744
QY 715 TATTGTGAGGCTGTATTAACAAGGTTTATGATCAATAAGACAGCGGGTACAGTGTCT 774
DB 745 CACTGTGTAAGTGTATGAACTGCTTTAGCAAAATTAATA-----GGCAGAGCGCT 798
QY 775 GAAGTTGTGCGAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATTT 834
DB 799 AAACATGAGGTGATCTATTAACCAATTCCTGAGAAATGACACTGGCGGTTTATGATGTT 858
QY 835 ATTGCTATATTTTCAACTTATGATTTTGAATAATATCCATTAGCAACAGTGTATGATTA 894
DB 859 GTTGCAATTATTTCCCAATTAATGACAAATACGTAACCAATGGAATGAAAGACAACTA 918
QY 895 ACTAGGAAATTTATACAGATCCAGTGGG 923
DB 919 ACAAGGAAATATATACAGATCCAGTGGG 947

```

Search completed: December 19, 2005, 13:47:56
Job time : 194.099 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:27:04 ; Search time 251.648 Seconds

(without alignments)
14261.593 Million cell updates/sec

Title: US-10-782-141-2

Sequence: 1 gtgaataatgaattctta.....atagttatttaccattaa 2019

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCBUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172.4	8.5	3468	US-09-001-982-9	Sequence 9, Appl1
2	172.4	8.5	3468	US-09-668-650-9	Sequence 9, Appl1
3	172.4	8.5	3471	US-09-002-285-71	Sequence 71, Appl1
4	172.4	8.5	3471	US-09-589-477-71	Sequence 71, Appl1
5	172.4	8.5	3471	US-10-099-285A-71	Sequence 71, Appl1
6	172.4	8.5	3726	US-09-001-982-11	Sequence 11, Appl1
7	172.4	8.5	3726	US-09-668-650-11	Sequence 11, Appl1
8	162.8	8.1	2407	US-09-661-322A-29	Sequence 29, Appl1
9	119.8	5.9	1959	US-09-661-322A-5	Sequence 5, Appl1
10	118.2	5.9	3934	US-08-100-709-3	Sequence 3, Appl1
11	118.2	5.9	3934	US-08-176-865-3	Sequence 3, Appl1
12	118.2	5.9	3934	US-08-474-038-3	Sequence 3, Appl1
13	118.2	5.9	3934	US-08-779-046-3	Sequence 3, Appl1
14	118.2	5.9	3934	US-08-881-340-3	Sequence 3, Appl1
15	116.8	5.8	3684	US-08-448-170-7	Sequence 7, Appl1
16	116.8	5.8	3684	US-08-961-803-5	Sequence 5, Appl1
17	116.8	5.8	3684	US-09-661-322A-62	Sequence 62, Appl1
18	112.4	5.6	4173	US-09-661-322A-37	Sequence 37, Appl1
19	111.8	5.5	1897	US-08-363-970-5	Sequence 37, Appl1
20	111.8	5.5	3471	US-09-002-285-73	Sequence 73, Appl1
21	111.8	5.5	3471	US-09-589-477-73	Sequence 73, Appl1
22	111.8	5.5	3471	US-09-661-322A-27	Sequence 27, Appl1
23	111.8	5.5	3471	US-10-099-285A-73	Sequence 73, Appl1
24	111.8	5.5	4344	US-08-532-547-4	Sequence 4, Appl1

25	111.8	5.5	4344	2	US-08-379-656B-4	Sequence 4, Appl1
26	111.8	5.5	4344	3	US-08-455-838-4	Sequence 4, Appl1
27	111.8	5.5	4344	3	US-09-019-809-4	Sequence 4, Appl1
28	111.8	5.5	4344	3	US-09-471-177-4	Sequence 4, Appl1
29	111.8	5.5	4344	3	US-09-220-806-4	Sequence 4, Appl1
30	110.8	5.5	1561	2	US-08-532-547-2	Sequence 2, Appl1
31	110.8	5.5	1561	2	US-08-379-656B-2	Sequence 2, Appl1
32	110.8	5.5	1561	3	US-08-455-838-2	Sequence 2, Appl1
33	110.8	5.5	1561	3	US-09-019-809-2	Sequence 2, Appl1
34	110.8	5.5	1561	3	US-09-471-177-2	Sequence 2, Appl1
35	110.8	5.5	1561	3	US-09-220-806-2	Sequence 2, Appl1
36	107.8	5.3	1607	3	US-08-286-870A-5	Sequence 5, Appl1
37	107.8	5.3	1946	3	US-08-286-870A-3	Sequence 3, Appl1
38	107.8	5.3	2965	2	US-08-460-570-1	Sequence 1, Appl1
39	107.8	5.3	2965	2	US-08-460-570-2	Sequence 1, Appl1
40	107.8	5.3	2965	3	US-08-286-870A-1	Sequence 1, Appl1
41	107.8	5.3	2965	3	US-08-286-870A-2	Sequence 2, Appl1
42	105.2	5.2	3507	2	US-08-315-468-3	Sequence 1, Appl1
43	104.4	5.2	4074	2	US-08-377-690-1	Sequence 1, Appl1
44	103.4	5.1	3414	2	US-07-973-320-3	Sequence 3, Appl1
45	101.8	5.0	1953	2	US-08-315-468-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-001-982-9
Sequence 9, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8589
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468

US-09-001-982-9

Query Match 8.5%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 161 GGGATCAGCTCGATATATAGTAACTATTTGGGACATACCTTATACATTTCTGCTGAAC 220
DB 158 GCGATGACGAAAAGAGAGATATCTTTGGGACAAACATAGTCTCTTTATACAGCAC 217
QY 221 CCGGTATAGGTGAATTCCTGTAATATTTT-----CAATATATAAACAACTGATTCCT 274
DB 218 CTCTCTTACTGGATTAATTTCAATAGTATAGACCTTATAGTAAAGTCTAGAGGTA 277
QY 275 CTCTGTGCAATCTGTGCGACACTTTCTATATGCTATTTAGTATCTATATTCGTAAG 334
DB 278 GTAGTGACATCATATGAGATTTGTATATATGATGCTATATCTATATTAATTAATTTAC 337
QY 335 AGGTAGACGAGACGCTGTTAGTGAAGGGGTGACATTTTGAAGGTAATGACTGCTT 394
DB 338 GGGTATAGTCAAGTGTTTTAATGATGAGATTCAGATTTTAATGTTCTGTACTCTAT 397
QY 395 ATCAAGATTAATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 439
DB 398 ACAGAACTATTTAGAGGCTCTGATAGCTGAAATTAAGAAATCTTAATCTGCTTCTG 457
QY 440 AATCAATCTTAATAAACTGCTGAGCTAGTAAAGCTTCAAGACGGGAAGAGATT 499
DB 458 AAGAACTCGCTACTCGTTTAAATGCGCAGCTCAGAAATTTGATAGAAATTTAAACCG 517
QY 500 TCACAACTTTTGAAGGCTCATTTATCAAGAGAAAGTGAATTTATTTATGCTTA 559
DB 518 GGTCTTTAAGAAATGGGCTCGTATGCTAGCAAAATGCCCCAAATTTATTTATTCCT 577
QY 560 CGATGTGCAAGCTGCAATGTGATTTATCTATTAAGGACGCAATTAATTAATTA 619
DB 578 CTCTTGAGACGCTGCAATTTTCCATTTATTAAGGATGCTACTAGATATGGCA 637
QY 620 AAGAAATGGGACATAGTGTGCAACCTTGTATCCAGGTCAGGAAACGATTTGTAAG 679
DB 638 CTAAATTTGGGGCTATACAAATGCTACACCTTTATTA-----ATTATCAAT 682
QY 680 AGCGTTTAAAGCGAAATTAAGATATCTAATTTGTGAGGTTGTTATACAGG 739
DB 683 CAAACTAGTAGGCTTATGAACTATATCTATTTGCTATGCTATGTAATGTAATGAG 742
QY 740 GTTTAGATCAGATTAAGCAGCGGGTAAAGTGTGCAAGTTTGTGCAATTTATTAAT 799
DB 743 GTTTCAACGAATTAAGCAACAGGACATAGTGTGCTACAGCTGTGTTAGATTTCA 802
QY 800 TTGCTGAGAAAGACCTTGGCGGTATTTGATATTAATTTGCTATATTTCCAACTAT 859
DB 803 ATGCTGAGAGATGACATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 862
QY 860 TTGAAAATATTCATTTAGCAACAGTGAAGTTAACTAGGAAATTTATACAGATTCAG 919
DB 863 TTACTATTAATCCCAATGAAACAGATTTTCAAGTTGATGAGGTCATTTATACAGAT 922
QY 920 TGGGATATTCAGGGGGAATTAATGTTGGGA 951
DB 923 TTGGTTTGTACATCTGATAGTCTTAGGGGA 954

RESULT 2

US-09-668-650-9
; Sequence 9, Application US/09668650
; Patent No. 6780408
; GENERAL INFORMATION:
; APPLICANT: Boesch, Hendrick J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

ADDRESSER: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-6689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-668-650-9

Query Match 8.5%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 161 GGGATCAGCTCGATATATAGTAACTATTTGGGACATACCTTATACATTTCTGCTGAAC 220
DB 158 GCGATGACGAAAAGAGAGATATCTTTGGGACAAACATAGTCTCTTTATACAGCAC 217
QY 221 CCGGTATAGGTGAATTCCTGTAATATTTT-----CAATATATAAACAACTGATTCCT 274
DB 218 CTCTCTTACTGGATTAATTTCAATAGTATAGACCTTATAGTAAAGTCTAGAGGTA 277
QY 275 CTCTGTGCAATCTGTGCGACACTTTCTATATGCTATTTAGTATCTATATTCGTAAG 334
DB 278 GTAGTGACATCATATGAGATTTGTATATATGATGCTATATCTATATTAATTAATTTAC 337
QY 335 AGGTAGACGAGACGCTGTTAGTGAAGGGGTGACATTTTGAAGGTAATGACTGCTT 394
DB 338 GGGTATAGTCAAGTGTTTTAATGATGAGATTCAGATTTTAATGTTCTGTACTCTAT 397
QY 395 ATCAAGATTAATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 439
DB 398 ACAGAACTATTTAGAGGCTCTGATAGCTGAAATTAAGAAATCTTAATCTGCTTCTG 457
QY 440 AATCAATCTTAATAAACTGCTGAGCTAGTAAACAGTTTCAAGACGGGAAGAGATT 499
DB 458 AAGAACTCGCTACTCGTTTAAATGCGCAGCTCAGAAATTTGATAGAAATTTAAACCG 517
QY 500 TCACAACTTTTGAAGGCTCATTTATCAAGAGAAAGTGAATTTATTTATGCTTA 559
DB 518 GGTCTTTAAGAAATGGGCTCGTATGCTAGCAAAATGCCCCAAATTTATTTATTCCT 577

QY 560 CGATGTGCAAGCTGCAAAATGCAATTATTACTATTAGGAGCGAGTTAAATATATAA 619
DB 578 CTTTGGGAGGCGCTGCAATTTTCCATTATTACTACTAGGAGTACTAGATATGGCA 637
QY 620 AAGATGGGGACTGTGTGTCACCGTTGTATCCAGGTCAGGAGAACTGATTTAGC 679
DB 638 CTAAATGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
QY 680 AGCGTTTAAAGCGAAATATAAGATATTAATTATTTGTTAGGGGTATATACAAG 739
DB 683 CAAACTAGTAGACTTATTAATTAATTAATTTGTTAGTTGTTAGTTAGTTAGTTAG 742
QY 740 GTTTAGTTCAGATTAAGACAGCGGGTACAGTGTGTAAGTTGTGCAAAATTTATAAT 799
DB 743 GTTTCACGAACTAAGACACAGGCGCACTAGTGTACAGCTTGGTTAGAAATTTCAATGAT 802
QY 800 TTGCTAGAAATGACCTTGGCGGTATTTGATATTATTGCTATATTTTCCAACTATGAT 859
DB 803 ATCTAGAGAGATGACATGATGATATTAGATATGATGATCAATTTTCAAGTCTGATA 862
QY 860 TTGAAAATATCCATTAGCAACAAGTATGATTAACTAGGAAATTTATACAGATCAG 919
DB 863 TTACTAATTAACCAATAGAAACAGATTTTCAGTTGAGTAGGGTCAATTTATACAGATCAA 922
QY 920 TGGATATTCAGGGGGAATTTAGTTGGAA 951
DB 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 3
US-09-002-285-71
; Sequence 71, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schiefel, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-002-285-71
Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
QY 161 GGGATCAAGTCTGGATATATGATCTTTGGGACATACCTTATPACATTTCTGTAGAAC 220
DB 158 GCCATGACGCAAAAAGAGCAGTATCTATTTGGGCAACCAATAGCTCTTATACAGACAC 217
QY 221 CCGGTATAGGTGAATCCCTGTAATTTT-----CAATATTAACAACTCATTCCT 274
DB 218 CTCTCTTACTGATTAATTTCAATAGTATATAGACCTTATAGGTAAAGTACTAGAGGTA 277
QY 275 CTCTGTGCAATCTGTGGCAGCACTTCTATATGTGATTTAGTATCTATATTCGTTAAAG 334
DB 278 GTAGTGAACAATCATATCAGATTTGTCTATATGTGACTTATATCTATATTTGATTTAC 337
QY 335 AGGTAGCAGAGCGTGTAAATGACGCGGTTGCAATTTTGAAGGTGAATGACCTT 394
DB 338 GGGTAAAGTACAGAGTGTAAATGATGAGGATTCAGATTTTAAATGTTCTGTACTTAT 397
QY 395 ATCAAGTTATTTATCTT-----ATTATCTTGAAGATTGGCTTACAGATA 439
DB 398 ACAGGAACATAATTAAGAGCTCTGATGATGCAATTAAGAAATCTTAATTTGCTTGTCTG 457
QY 440 ATCAAAATCTTAATAAACTTGCTGACGTAGTTAAACAGTTCACAGCAAGGAAAGAT 499
DB 458 AAGAACTCCGTACTCGTTTATGAAATGCCGACCTCAGAAATTTGATAGATTTTAAACCCGAG 517
QY 500 TCACTAAACTTTTACAGAGGCTATTTATCAAGACAGAAAGTGAATATTTATTTGCTTA 559
DB 518 GGTCTTTAAAGAAATGGGCTCGTTAGCTGACAAATATGCCAAATTTATTTATTAACCTT 577
QY 560 CGATGTGCAAGCTGCAAAATGTCATTTATTAATTAATTAAGGAGCGCAATTAATATAA 619
DB 578 CTTTGGAGCGCTGCAATTTTCCATTATTTACTATCAAGGATGCTACTAGATATGCA 637
QY 620 AAGATGGGGACTAGTGTGCCACCGTTGATCAGGGTCAAGGAGAACTGATTTAGC 679
DB 638 CTAAATGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
QY 680 AGCGTTTAAAGCGAAATATAAGATATTAATTATTTGTTAGGGGTATATACAAG 739
DB 683 CAAACTAGTAGAGCTTATTAATTAATTAATTTGTTAGTTGTTAGTTAGTTAGTTAG 742
QY 740 GTTTAGTTCAGATTAAGACAGCGGGTACAGTGTGTAAGTTGTGCAAAATTTATAAT 799
DB 743 GTTTCACGAACTAAGACACAGGCGCACTAGTGTCTACAGCTTGGTTAGAAATTTCAATGAT 802
QY 800 TTGCTAGAAATGACCTTGGCGGTATTTGATATTATTGCTATATTTTCCAACTATGAT 859
DB 803 ATCTAGAGAGATGACATGATGATATTAGATATGATGATCAATTTTCAAGTCTGATA 862
QY 860 TTGAAAATATCCATTAGCAACAAGTATGATTAACTAGGAAATTTATACAGATCAG 919
DB 863 TTACTAATTAACCAATAGAAACAGATTTTCAGTTGAGTAGGGTCAATTTATACAGATCAA 922
QY 920 TGGATATTCAGGGGGAATTTAGTTGGAA 951
DB 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 4
US-09-589-477-71
; Sequence 71, Application US/09589477
; Patent No. 6570005

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEO ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-589-477-71

Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4,4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGAATCATCTCGGATATGTAATTTGGGACATACCTTAACAATTTCGCTGAGAC 220
158 GCGATGCGAGAAAGACAGTATCTATTGGGACACCATAGTCTCTTATACAGCAC 217
221 CCGGTATAGTGGAAATCTGTATATTTT-----CAATATTAACAACCTATCCGT 274
218 CTCTCTTACTGATTAATTTCAATAGTATATGACCTTAAGGTAAGTCTAGAGAGTA 277
275 CTTCGTGATCATCTGTGGACGACTTCTATATGTGATTTAGTATCTATTAATTCGTAAG 334
278 GTAGTGGACATCATCATGATTTGCTATATGTGACTATATATCATATTAATGATTTAC 337
335 AGGTAGACGAGCGGTGTAGTACGCGGGTTCAGATTTTGAAGGTAAGTACGCTT 394
338 GGGTATGTCAGAGTGTTTAAATGATGAGATTGCGATTTTAATGTTCTGTACTCTTAT 397
395 ATCAAGTATTAATCTT-----ATTATCTGAGGATTCGCTTACAGATA 439
398 ACAGGACTATTTAGAGGCTCTGATAGCTGAGATTAAGAACTTAATTCGCTTCTGCTG 457
440 AATCAATCTTAATAAACTTGCTGACGTAGTTAAACAGTTCCAAGCAGGGAAGAGATT 499

458 AAGAACTCCGTAATCTGTTTAGAATCGCGACTCAGAAATTTGATAGAAATTTAAACCCGAG 517
500 TCACTAACTTTAGCAGGGCTATTAATCAAGACAGAACTGAATATTAATTAATTCGCTTA 559
518 GGTCTTTAAGCATGTGTGCTGCTTGAAGTAAATGCCAAATATTAATTAATTAATTCCTT 577
560 CGTATGTGACCTGCAATATGTCATTTTCTATTAAGGACGAGTAAATTAATAA 619
578 CTTTGCGAGCGCTGATTTTTCATTAATTAATCTAAAGGATGCTACTAGATATGCGCA 637
620 AAGATGAGGAGTATGTGTCCACCGTGTATCCAGGCTCAGGAGAACATGATTTGTAAG 679
638 CTAATTTGGGGCTATATACATGCTACACCTTTATA-----ATTATCAAT 682
680 AGCGTTAAAGCGAAATTAAGATATTAATTAATTTGTTAGGCTGTATTAACAG 739
683 CAAACTAGTAAAGCTTATTTGAACATATATCATGATTAATGCTTACATTTGTTAATCAG 742
740 GTTTAGATCATAGACAGCGGGGTACAGGCTGAAGTGTGCAATTTAATAAT 799
743 GTTTCAAGCACTAAGACAGAGGCTAGTGTACGCTTGTTAGAAATTCATAGAT 802
800 TTGTAAGAAATGACGTGTGCGGTATTTGATTAATTTCTAATTTCCAACTTATGATT 859
803 ATGTAAGAGATGATGATGATGATTAATGATTAATGATACATCATTTCAAGCTTGATA 862
860 TTGAAAAATATCATTTAGCAACAAGTGTAGATTAACTTGGGAAATTTATACAGATCCAG 919
863 TTACTAATTAATCCCAATAGAAACAGATTTTCAGTGTAGTGGGTCAATTTATACAGATCAA 922
920 TGGGATATTCAGGGGGAATTAATGTTGGGAA 951
923 TTGTTTGTATCATGCTAGTACTTTAGGGGA 954

RESULT 5
US-10-099-285A-71
Sequence 71, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285A-71

Query Match 8.5%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 4.4e-33;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGATCAGTCTCGATATAGTAACTATGGGACATACCTTATCAATTCCTGCTAGAC 220
158 GCGATGAGCAAAAGAGACATCTATGGGACACCAATGCTCTTATCAGACAC 217
221 CCGGTATAGGTGGAATTCCTGATATTTT-----CAATATAAACAACCTATCCGT 274
218 CTCTCTTACTGAGTATTAATTAATGATGACCTTATAGTAAAGTCTAGAGATA 277
275 CTCTGTCATCTGTCGACGACCTTCTATATAGTAACTTATAGTATCTATATCGTAAG 334
278 GTAGTGACATTCATATCAGATTTGCTATATGACTTATATCTATATTAATTTAC 337
335 AGGTAGACGAGCGGTGTAAGTACGCGGTGACATTTGAGGCTGAATGACTGCT 394
338 GGGTAATCAGAGGTTTAAATGATGGATGACATTTTAATGCTTCTGATCTTAT 397
395 ATCAAGTTATATCTTC-----ATTATCTGAGATTCGCTTACAGATA 439
398 ACAGAACTATTTAGAGCTCTGATAGCTGGAATTAAGAACTTAATTCGCTTCTGCTG 457
440 AATCAATCCTAAGAACTGCTGACGATGTAACGTTCCAGACGCGGAAGAAAT 499
458 AAGAACTCCGACTCGTTTGAATTCGCCGACCTAGAAATTTGAATTTTAAACCGGAG 517
500 TCACTAACTTTTACGAGGCTCATTATCAGACAGAAAGTGAATATTTATTTGCTTA 559
518 GGTCTTTAAGAAATGGGCTCGTTAGTACAGAAATGCCAAATTTATTTATTA 577
560 CGTATGCAAGCTGCAATGTCATTTATTTAAGGACGCGATTAAATATAA 619
578 CTTTGGAGCGCTGCAATTTTCCATTTATTTACTACTAAGGATGCTACTAGATATGCA 637
620 AAGAATGGGACCTAGTGTCCACGTTGATCCAGGGTCAAGGAGAAAGATGTTAGAC 679
638 CTATTTGGGGCTATTAACAATGCTACACCTTTATTA-----ATTATTAAT 682
680 AGCGGTAAAAAGCAAAATATAAGATATACTAATTTATTTGAGGCTGATTAACAAG 739
683 CAAAACATAGTAGCTTATTAATTAATTAATTTATTTGCTGATTTGATTAATGAG 742
740 GTTTAGTACAGATTAACAAGCGGGGTACAAGTCTGAAGTTTGTCAAAATTAATAAT 799
743 GTTTCACGAACTAAGACAAAGAGGCACTAGTCTAGAGCTTGTGAAATTTCAATGAT 802
800 TTGCTAGAAAGTACGTTGGCGGTATTTGATTTATTTGCTCAATTAAT 859
803 ATCTAGAGCATACATTAATGATTTATTAATTAATTAATTAATTTCAAGTCTTATA 862
860 TTGAAAATATATCCATTAGCAACAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 919
863 TTACTAATTAATCCCAATTAAGAAATGATTTTCAAGTGAAGTGAAGTGAAGTGAAG 922
920 TGGATATTTACAGGGGGAATTAATTTAGTTGGGA 951

Db 923 TTGTTTGTACATCGTAGTACTTAAAGGGA 954

RESULT 6

US-09-001-982-11
Sequence 11, Application US/09001982
Patent No. 6204246

GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/001,982

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/602,737

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3726 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3726

US-09-001-982-11

Query Match 8.5%; Score 172.4; DB 3; Length 3726;

Best Local Similarity 54.2%; Pred. No. 4.5e-33;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

161 GGGATCAGTCTCGATATAGTAACTATGGGACATACCTTATCAATTCCTGCTAGAC 220
158 GCGATGAGCAAAAGAGACATCTATGGGACACCAATGCTCTTATCAGACAC 217
221 CCGGTATAGGTGGAATTCCTGATATTTT-----CAATATAAACAACCTATCCGT 274
218 CTCTCTTACTGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 277
275 CTCTGTCATCTGTCGACGACCTTCTATATAGTAACTTATAGTATCTATATCGTAAG 334
278 GTAGTGACATTCATATCAGATTTGCTATATGACTTATATCTATATTAATTTAC 337
335 AGGTAGACGAGCGGTGTAAGTACGCGGTGACATTTTGAAGTGAATGACTGCT 394
338 GGGTAAGTCAAGAGTGTAAATGATGAGATGCAATTTTAATGCTTCTGATCTTAT 397
395 ATCAAGTTATATCTTC-----ATTATCTGAGATTCGCTTACAGATA 439

Db 398 ACAGAACTATTAGAGGCTCTGGATGCTGATGAATAAGATCCGAATTCCTGCTTCG 457
 Qy 440 AATCAATCTTAAAAAAGCTGCTGAGCTACTTAACAGCTTCCAGCAGCGGAAGAAATT 499
 Db 458 AAGAACTCCGCTACTCGTTTGAATGCCCACTCAGATTTGATGATTTTAAACCGAG 517
 Qy 500 TCACATACTTTAGCAGGCTCATTTATCAAGAGAAAGTGAATTTATTTATTTGCGTA 559
 Db 518 GGTCTTTAAGAAATGGGCTCGTACCTAGTACGAAATGCCAAATTTATTTACCTT 577
 Qy 560 CGATGTGCAAGCTGCAATATGCAATTTATTTATTTAGGAGCAGTTAAATATATAAA 619
 Db 578 CTTTGGAGCGCTGCAATTTTCCATTTATTTACTAATAGGATGCTACTAGATATGGCA 637
 Qy 620 AAGAAATGGGACATAGTGTGCAACCTTGTATCCAGGCTCAGGAGACATGATTTGACG 679
 Db 638 CTAAATGGGGGCTATACAAATGCTACACCTTTTATTA-----ATTATCAAT 682
 Qy 680 AGCGTTAAAGCGAAATTAAGATATCTAATTTGTGTAGGGGTGATTAACAG 739
 Db 683 CAATACTAGTAGCTTATTTGAATATATCTGATTTTGGTACATGATTAATCGAG 742
 Qy 740 GTTTAGATCAGATPAGACAGCGGGTACAAAGTGTGAAGTTTGGTCAAAATTTAATPAA 799
 Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTGTACAGCTGGTTAGAAATTTCAATGAT 802
 Qy 800 TTGGTAGAAATGAGCTGGCGTATGGATTTATTTGCTATATTTCCAACTTAATGAT 859
 Db 803 ATGTGAGAGATGACATGATGATTTAGATATAGATCATCATTTCAAGCTTGATA 862
 Qy 860 TTGAAAAATATCATTTAGCAACAAGTGTAGATTAACTAGGAAATTTATACAGATTCAG 919
 Db 863 TTACTAATTTCCCAATAGAAACAGATTTTCAAGTTGAGTATGATTTATACAGATCCAA 922
 Qy 920 TGGGATATTCAAGGGGGAATTTATGTTGGGA 951
 Db 923 TTGGTTTGTACATCTGATGATGCTTTAGGGGA 954

RESULT 7
 US-09-668-650-11
 ; Sequence 11, Application US/09668650
 ; Patent No. 6780408
 ; GENERAL INFORMATION:
 ; APPLICANT: Bosch, Hendrick J.
 ; TITLE OF INVENTION: Hybrid J.
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: No. 6780408artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/668,650
 ; FILING DATE: 22-Sep-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/001,982
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/602,737
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8687
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3726
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-668-650-11
 Query Match 8.5%; Score 172.4; DB 3; Length 3726;
 Best Local Similarity 54.2%; Pred. No. 4,5e-33;
 Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
 Qy 161 GGAATCACTCTCGATATAGTAACTTTGGGACATCTTATACAAATCTTGCTAGAAC 220
 Db 158 GCGATGCAACAAAGAGCAGATCTATTTGGGACAAACATGCTCTCTTATCACAGCAC 217
 Qy 221 CCGATATAGTGAATTCCTGATATATTTT-----CAATATTAACAACATCATTCGCT 274
 Db 218 CTTCTCTTATCTGATTAATTTCAATATGATATGACCTTATAGCTTAAGTACTAGAGGTA 277
 Qy 275 CTTCTGCTCAATCTGTGGCAGCACTTCTATATGATTTAGTATCTATTAATTCGTAAAG 334
 Db 278 GTATGAGCAATTCATATACAGATTTGTCTATATGATCTTATATCTATTTATGATTTAC 337
 Qy 335 AGGTAGCAGACGCGTTTAACTGACAGGGGTGCAATTTTGAAGGTGAATAGATCGCT 394
 Db 338 GGTATAGTCAGAGTGTTTAAATGATGGATGCAAGATTTTAATGATGCTTAT 397
 Qy 395 ATCAAGATATTTATCTTC-----ATTATCTGAGATTTGGCTTACAGATA 439
 Db 398 ACAGAACTATTAGAGGCTCTGATAGCTGAAATTAAGATCTTAATTCGTTCTGCTG 457
 Qy 440 AATCAATCTTAAAAAAGCTGCTGACGATTTAAACAGTTCCAGCAGCGGAAGAAATT 499
 Db 458 AAGAACTCCGCTACTCGTTTGAATGCCCACTCAGATTTGATGATTTTAAACCGAG 517
 Qy 500 TCACATACTTTAGCAGGCTCATTTATCAAGAGAAAGTGAATTTATTTATTTGCGTA 559
 Db 518 GGTCTTTAAGAAATGGGCTCGTACCTAGTACGAAATGCCAAATTTATTTATTTACCTT 577
 Qy 560 CGATGTGCAAGCTGCAATATGCAATTTATTTATTTAGGAGCAGTTAAATATATAAA 619
 Db 578 CTTTGGAGCGCTGCAATTTTCCATTTTATTTACTAATAGGATGCTACTAGATATGGCA 637
 Qy 620 AAGAAATGGGACATAGTGTGCAACCTTGTATCCAGGCTCAGGAGACATGATTTGACG 679
 Db 638 CTAAATGGGGGCTATACAAATGCTACACCTTTTATTA-----ATTATCAAT 682
 Qy 680 AGCGTTAAAGCGAAATTAAGATATCTAATTTGTGTAGGGGTGATTAACAG 739
 Db 683 CAATACTAGTAGCTTATTTGAATATATCTGATTTTGGTACATGATTAATCGAG 742
 Qy 740 GTTTAGATCAGATPAGACAGCGGGTACAAAGTGTGAAGTTTGGTCAAAATTTAATPAA 799
 Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTGTACAGCTTGTGTTAGATTTATCATGAT 802
 Qy 800 TTGGTAGAAATGACGTTGGCGTATTTGATATTTATTTGCTATTTTCCAACTTAATGAT 859
 Db 803 ATGTGAGAGATGACATGATGATTTAGATATAGATCATTTTCAAGCTTGATA 862
 Qy 860 TTGAAAAATATCATTTAGCAACAAGTGTAGATTAACTAGGAAATTTATACAGATTCAG 919
 Db 863 TTACTAATTTCCCAATAGAAACAGATTTTCAAGTTGAGTATGATTTATACAGATCCAA 922
 Qy 920 TGGGATATTCAAGGGGGAATTTATGTTGGGA 951

Db 923 TTGGTTTGTACATCGTAGTACTTGTAGGGGA 954

RESULT 8

US-09-661-322A-29
Sequence 29, Application US/09661322A
Patent No. 6593293
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupa, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
LENGTH: 2407
SEQ ID NO 29
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-09-661-322A-29

Query Match 8.1%; Score 162.8; DB 3; Length 2407;
Best Local Similarity 53.4%; Pred. No. 9,8e-31;
Matches 433; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

QY 161 GGGAAATCAGTCTCGAATATGTAATCTATTGGACATACCTTATCAATCTTGTAGAAC 220
DB 158 GCGATGACGAGAAAAGACAGTATCTATTGGACAACCATGCTCTCTTATCACAGCAC 217
QY 221 CCGGTATAGGTGGAATCCCTGATATTTT-----CAATATTAACAACCTACCTCCGT 274
DB 218 CTCTCTTACTGATTAATTAATTAATGATTAATGACCTTAATAGTAAAGTACTAGAGATA 277
QY 275 CTCTGTGCAATCTGTGACAGCACTTCTATATGATTAATGATTAATGATTAATGATTAATG 334
DB 278 GTATGACAAATCATATCAGATTTGTCTATATGTGCTTATATCTATATTTATTTATTTAC 337
QY 335 AGGTAGACGAGCGGTGTAATGACGCGGTGTCAGATTTTGAAGGTGAATGACCTCT 394
DB 338 GGGTAAGTACAGAGTTTAAATGATGAGATGTCAGATTTTAATGTTGTACTCTTAT 397
QY 395 ATCAAGTATTAATCTT-----ATTATCTTGAGGATTTGCTTACAGATA 439
DB 398 ACAGAACTATTAAGAGCTCTGATAGCTGGAATTAAGAACTTAATTTGCTTCTGCTG 457
QY 440 AATCAATCTTAATAAACTTGCTGACGTAATTAACAGTTCAAGCACGGGAAGAGATT 499
DB 458 AAGAACTCCGTATCTGTTTGAATCCCGACCTCAGATTTGATAGAAATTTTAAACCGGAG 517
QY 500 TCACTAACTTTTACGAGGTCATTAACAAGCAAGAGCTGAATTAATTTATTTGCTTA 559
DB 518 GGTCTTTAACGAATGGTGGCTCGTTAGCTAGCAAAATGCCCCAAATTTATTTATTA 577
QY 560 CGTATGTCAGAGTCGCAATGTGATTTATTTACTTATTAAGGACGCGTTAATATTA 619
DB 578 CTTTGTGAGCGCTGCAATTTTTCATTTATTTACTACAGGAGTCTTACATGATATGCA 637
QY 620 AAGATAGGGACTAGTGTGTCAACGTTGATCCAGGGTCAGGGAAGATGATTTGTAACG 679
DB 638 CTATTTGGGGCTTATACATGCTACACCTTTAATA-----ATTATCAAT 682
QY 680 AGCGTTTAAAGCGAAATTAAGAGTATTAATTAATTTGTTAGGGTGTATTAACAGG 739
DB 683 CAAAACATAGTAGACTTATGAACTATATTACTGATTTTGGGTACATTTGGGATATAGAG 742
QY 740 GTTTAGATCAGATTAAGCAGCGCGGTACAGTGTGTAAGTTTGTCCAAATTTTAATTAAT 799

DB 743 GTTCAACCGAATTAAGAACGAGGCGCTTAGTCTACAGCTTGGTTAGAAATTTATCATGAT 802
QY 800 TTGTAAGAAATGACGTTGCGGTATTTGATATTAATTTGCTAATTTTCAACTATGATT 859
DB 803 ATCGAGAGAGATGACATTTATGGAATTAAGAAATAGATCATTTTCAAGCTTGATA 862
QY 860 TTGAAATAATATCCATTTAGCAACAGTGTAGAGTTTACTAGGAAATTTATACATGATCCAG 919
DB 863 TTACTATTTACCAATTAAGAAACAGATTTTTCAGTTGAGTGGGTATTTATACATCCAA 922
QY 920 TGGATATTAAGGGGGAATTAATGTTGGGA 951
DB 923 TTGGTTTGTACATCGTAGTACTTGTAGGGGA 954

RESULT 9

US-09-661-322A-5
Sequence 5, Application US/09661322A
Patent No. 6593293
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupa, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 1959
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-09-661-322A-5

Query Match 5.9%; Score 119.8; DB 3; Length 1959;
Best Local Similarity 55.0%; Pred. No. 5e-20;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

QY 435 AGATAAATCAATCTTAATAAACTTGCTGACGTAATTAACAGTTTCAAGCAGGGAAGA 494
DB 411 AGATAACCGAATGATGCAAGATCAAGAGCATTAATTTGAGCGCTATGCTTTAGA 470
QY 495 AGATTTCATTAATCTTTAGCAGGTCATTAACAAGCAAGAGCTGAATTAATTAAT 554
DB 471 ACTTGACATTAATCTAGCTATATCCGCTTTGAGAAATGCAAAATGAAAGATTCATTAAT 530
QY 555 GCTTACGTATGTCAGAGTCGAATGTGATTAATTAATTAATTAATTAATTAATTAATTA 614
DB 531 AATGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGACGACATCCCTTT 590
QY 615 TAAAAAAGAAATGGGGAATAGTGTGTCACCTGTTTATCCAGGTCAGGGAAGCTGAT 674
DB 591 TGGTAGTAATGGGGATGGCATCTTCCGATGTTAACAA-----TA 632
QY 675 TAAACGCGGTTTAAAGCGAATAATTAAGAGTATTAATTAATTTGTTAGGGTGTATTA 734
DB 633 TTACCGAAGAACCAATCAGATTAACAAGGAATATTTCAACATTTGCGTACAAATGTA 692
QY 735 CAAGGTTTATGATCAGATTAAGACAGCGGCTACAGTGTGTAAGTTTGGTCAAAATTTAA 794
DB 693 TACAGGGCTTAATAATTAAGA-----GGCAAAATGCTGAAGATTGTTGGGCTATTA 746
QY 795 TAAATTTCTGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATATTTTCAACTTA 854
DB 747 TCAATTCGTAAGACCTTAACGTTAGGGGTATTTAGATTTAGATCCCTATTTCCCAAGCTA 806
QY 855 TGATTTGAAATAATTCATTCATTAAGCAACAGTGTAGATTAACTAGGGAATTTATACAG 914
DB 807 TGATTAATCGCATTTATTCATTAATATCGAGTGTCTCAGTTTAAACAGGAATTTATACAG 866

NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-176-865-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

435 AGATTAATCAATCTTAAATACTTCTGACGTAAGTTAAACAGTCCAGACGGAGA 494
492 AGATTAACGGAATGATCAAGATCAAGACATTAATCTTGAGCGCTATGTTCTTAGA 551
495 AGATTTCATTAATCTTTAGCAGGGTCAATTAAGACAGAACTGAAATATATAT 554
552 ACTTGATTAATCTTCTGCTATACCGCTTTAGAAATGAAATGAAAGTCCATTAAT 611
555 GCTTACGTAATGTAAGCACTGCAATGCAATTTATTAATTAAGACGAGTTAATA 614
612 AATGTAATATGCTCAAGCTGCAATTTACACCTATTTATTAAGACGATCCCTTT 671
615 TAAAAAAGATGGGACTAGTGTCCACCGTGTATCCAGGTCAGGGAACCTGAT 674
672 TGGTAGGAATGGGGATGGCATCTCCGATGTTAACCA-----TA 713
675 TAACGAGCGTTAAACGCAAAATAAAGATATATATTTGTAGGGGTATTA 734
714 TTACCAAGAACCAATCAATATACAGAGAAATATTAACCATTTGCGTACATGTATTA 773
735 CAAGGTTTATGATCAGATTAAGACAGCGGTAAGTGTGAAAGTTTGTGAAATTTAA 794
774 TACGGGCTTAATTAATCTTAAGA-----GGACAAATGCTGAAGTTGTTGCGTATTA 827
795 TAAATTTGTAAGAAATGACGTTGGCGTAATGTAATTAATGCTATTTCCACTTA 854
828 TCAATTCGTAAGACCTTAACGTTAGGGGATTAATGATTTAGTACCCATTTCCAACTA 887
855 TGATTTGAAAAATATTCATTAAGCAACAGTGTAGATTAATCTAGGAAATTTATCAGA 914
888 TGATTAATCGCACTTATCAATCAATACAGAGTGTCAAGTTAAACAGAAATTTATACAGA 947
915 TCCAGTGGATATTCAGGGGAAATTAATGTTGGAAACGTTTATTAAGCTTTAT 969
948 TCCATTTGGAGAACCAATGACCTTCAGAGATTTGCAAGTACGAATGTTTAT 1002

RESULT 12

US-08-474-038-3
Sequence 3, Application US/08474038
Patent No. 5679343
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESS: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,038
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865

FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709

FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:

NAME: Egoft, Christopher
REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs

TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS
LOCATION: 67..3756

FEATURE:

NAME/KEY: misc feature
LOCATION: 2253..2272

US-08-474-038-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

435 AGATTAATCAATCTTAAATACTTCTGACGTAAGTTAAACAGTCCAGACGGAGA 494
492 AGATTAACGGAATGATCAAGATCAAGACATTAATCTTGAGCGCTATGTTCTTAGA 551
495 AGATTTCATTAATCTTTAGCAGGGTCAATTAAGACAGAACTGAAATATATAT 554
552 ACTTGATTAATCTTCTGCTATACCGCTTTAGAAATGAAATGAAAGTCCATTAAT 611
555 GCTTACGTAATGTAAGCACTGCAATGCAATTTATTAATTAAGACGAGTTAATA 614
612 AATGTAATATGCTCAAGCTGCAATTTACACCTATTTATTAAGACGATCCCTTT 671
615 TAAAAAAGATGGGACTAGTGTCCACCGTGTATCCAGGTCAGGGAACCTGAT 674
672 TGGTAGGAATGGGGATGGCATCTCCGATGTTAACCA-----TA 713
675 TAACGAGCGTTAAACGCAAAATAAAGATATATATTTGTAGGGGTATTA 734
714 TTACCAAGAACCAATCAATATACAGAGAAATTTTAACCATTTGCGTACATGTATTA 773
735 CAAGGTTTATGATCAGATTAAGACAGCGGTAAGTGTGAAAGTTTGTGAAATTTAA 794
774 TACGGGCTTAATTAATCTTAAGA-----GGACAAATGCTGAAGTTGTTGCGTATTA 827
795 TAAATTTGTAAGAAATGACGTTGGCGTAATGTAATTAATGCTATTTCCACTTA 854
828 TCAATTCGTAAGACCTTAACGTTAGGGGATTAATGATTTAGTACCCATTTCCAACTA 887
855 TGATTTGAAAAATATTCATTAAGCAACAGTGTAGATTAATCTAGGAAATTTATCAGA 914
888 TGATTAATCGCACTTATCAATCAATACAGAGTGTCAAGTTAAACAGAAATTTATACAGA 947
915 TCCAGTGGATATTCAGGGGAAATTAATGTTGGAAACGTTTATTAAGCTTTAT 969
948 TCCATTTGGAGAACCAATGACCTTCAGAGATTTGCAAGTACGAATGTTTAT 1002

RESULT 13

US-08-779-046-3
Sequence 3, Application US/08779046
Patent No. 5854053
GENERAL INFORMATION:

APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S. M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panltch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-779-046-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

435 AGATAATCAATCTTAAAAAAGTCTGACGTAAGTTAAACAGTCCAGCAGGAGAGA 494
492 AGATAACCGAAATGATCAAGATCAAGACATTAATCTTGAGGCGTATGTGCTTAGA 551
495 AGATTCACCTAACTTTACAGAGGTATTAACAGCAGAAAGCTGAATATATATAT 554
552 ACTTGACATTACTACGTCTATACCGCTTTTCAGAAATCGAAAGAAAGTTCCATTA 611
555 GCCTAGCTATGTCAGAGCTCAAAATGTCATTTATTAAGGAGCGCAGTTAAATA 614
612 AATGCTATATGCTCAAGCTGCAAAATTTACACCTATTTTATTGAGAGACCAATCCCTTT 671
615 TAAAAAAGATGGGAGCTAGTGTGTCCACCGTTGTATCCAGGCTCAGAGAGAACTGATTG 674
672 TGGTAGAATGGGGAGTGCATCTTCGATGTTAACCA-----TA 713
675 TAAAGAGCGGTTAAAGCGAAATTAAGATATACATTAATTTGTAGGTGCTATTA 734
714 TTACCAAGAAACAAATCGATATACAGAGAAATTTTAAACATTTGCGTACAAATGATTA 773
735 CAAGGTTTATGATCAGATAAGACAGCGGGTACAAAGTGTGAAGTTTGTGGAATTTAA 794

774 TACAGGCTTAATTAAGT-----GGACAAATGCTGAAGTTGGTCCGTATTA 827
795 TAAATTCGTAGAGAAATGACGTGGCGGTATGATATTAATGCTATTAATTTCAACTTA 854
828 TCAATTCGTAGAGAACTTAAGTTAGGGGTATTAAGTTAGAGCCATATCCCAAGCTA 887
855 TGAATTTGAAAATATCCATTGCAACAGTGTAGAGTTAACTAGGAAATTTATACGA 914
888 TGAATTCGCACTTATCCAAATGACAGTGTCTCAGTTAACAGAAATTTATACGA 947
915 TCAGTGGATATTAAGGGGAAATTAATGTTGGGAAACGTTTATTAAGCTTAAT 969
948 TCAATTTGGAGAAACAAATGACCTTCAGAGATTTCAGAGTACGAATTTGTTAAT 1002

RESULT 14
US-08-881-340-3
Sequence 3, Application US/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panltch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-881-340-3

Query Match 5.9%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 1.6e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;


```

QY 435 AGATAATCAATCTTAAAAAAGTCTGAGCTACTTAACAGTTCCAGACGGGAGA 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 AGATTAACCGAAATGATCGAATATCAAGAGCATTAATCTTGACGGCTATGTCCTTAGA 551
QY 495 AGATTTCACCTAACTTTTACAGGGGTCAATTAACAAGCAGAAAGCTGAAATATATATT 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 ACTTGACATTAATCTACTGCTATACCGCTTTTCAAGATTAAGAAATAGAGTTCCATTAAT 611
QY 555 GCGTACGTATGTCAGAGCTGCAAAATGTCATTTATTAATTAAGAGCAGCAATTAATA 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 AATGTATATGCTCAAGCTGCAAAATTAACCTATTAATTAATTAAGAGCAGCATCCCTTT 671
QY 615 TAAAAAAGATGCGGACCTAGTGTCCAACCTGATTCAGAGGTCAGGAGAACTGATG 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 TGTAGTGAATGGGAGATGGCATCTTCGATGTAAACCA-----TA 713
QY 675 TAAACAGCGGTTAAAGAGAAATTAAGATTAATTAATTAATGTTGAGGGGTGTTAA 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 714 TTACCAAGAACAAATCGATATTAACAGAGAAATTTTCAACATTCGTAATGTAATA 773
QY 735 CAAGGTTTATGATCAGATTAAGACAGCGGCTACAGTGTGAGTTTGTGCAAAATTTAA 794
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 774 TAGAGGCTAAATTAACCTTAAGA-----GGGCAAAATGCTGAAGTGTGCGGTATTA 827
QY 795 TAAATTTCTGAGAAATGACGTTGGCGGTATTTGATTAATTAATTTTCAACTTA 854
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 TCAATTCCTGAGAGACCTTAACGTTAGGGGTATTAATTAATTAATTCCTATCCAACTA 887
QY 855 TGAATTTGAAATAATCAATTAAGACAGAGTGTAGCTTAATTAATTAATTAATTAACA 914
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 888 TGAATCTGCACTTATCCAAATCAATTAAGAGTGTCACTTAACAAGAAATTTTAACA 947
QY 915 TCCAGTGGATTAATCAAGGGGAAATTAATGTTGGGAAAGCTTTTGAAGCTTAAT 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 948 TCCATTTGGGAGAACAAATGCACTTCAGATTTTGAAGTGAAGTGAATGCTTAAT 1002

```

```

RESULT 15
US-08-448-170-7
; Sequence 7, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Steiman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.C. PSI58C, Active Against Lepidopteran Pests, and Genes
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247

```

```

; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-170-7
Query Match 5.8%; Score 116.8; DB 2; Length 3684;
Best local Similarity 55.0%; Pred. No. 3.4e-19;
Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;
QY 406 TATCTCATTAATCTTGAGATTGGCTTACGATTAATCAATCTTAAAAAAGTCTGAC 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 TATCAACAGCTTGAAGATTGGCTAGAAAACCGTATGATCAAGAACAGAAAGTGT 459
QY 466 GTAGTTAAACAGTTCACAGACGGAAGAAAGATTTCCTAACTTTTACAGAGGCTATTA 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 CTTTATTAACCAATATATAGCTTAGAACTTATTTCTTAATGCGATGCCGCTTTTGCA 519
QY 526 TCAAGACAGAAAGCTGAAATTAATTAATGCTTACGATGTCAGAGTGTGCAATGTCAT 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 ATTAGAAACCAAGAAATTCATTATTAATG--GTAATGCTCAAGCTGCAAAATTTAC 576
QY 586 TTTATTAATTAAGGAGCAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 CTATTAATTAATTAAGAGATGCTCTCTTTTGTAGTGAATTTGGCTTATCACTCCAGAA 636
QY 646 TTGATTCAGAGGTCAAGGAGAACTGATTTGTAAGAGCGGTTAAAGCGAAATTAAGAG 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 ATTCAAG-----TTATTAAGAGCGCAATGCAAAAACAGAGAA 678
QY 706 TATCTAATTAATTTGTAGGGGTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGCT 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 TATTCGATTAATTTGCGCAAGATGTATTAATACGGGTTTAATTAATTTGAGA-----GGG 732
QY 766 ACAAGTCTGAAGTTGGTGAATTAATTAATTTTGTGAGAAATGACGTTGGCGGTA 825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 733 ACAAAATGCTGAAGTTGGTGAATTAATTAATTTTGTGAGAAATGACGTTAGAGTA 792
QY 826 TTGATTAATTAATTTCAATTTCAATTTGATTTTGAATAATTAATTAATTAATTAATTA 885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 793 TTGATCTAGTGAACATTTCCAGAGCTATGACAGCGGTGTTTATCAATGAATTAACAGT 852
QY 886 GTAGAGTTAATCTAGGAAATTTATTAACAGATCCAGTGAATTAATTAATTAATTAAT 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 853 GTCATTAATTAACAAGAAATTTATTAACAGATCCAAATGGAGAACAAATGCACTTCA 912
QY 946 TGGGAACGTTTATTAATTTAT 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 913 TTTGCAAGTACGAATGCTTAAT 936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: December 19, 2005, 13:03:21
Job time : 256.648 secs

Handwritten text, possibly a signature or date, oriented vertically.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:29:27 ; Search time 1166.77 Seconds
(without alignments)
15202.512 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataatcatgtt.....atagttatcatcaatcaa 2145

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2145	100.0	2145	US-10-782-141-1	Sequence 1, App1
2	2019	94.1	2019	US-10-782-141-2	Sequence 2, App1
3	2010	93.7	2010	US-10-782-141-4	Sequence 4, App1
4	855	39.9	5980	US-10-781-979-1	Sequence 1, App1
5	747.2	34.8	2082	US-10-781-979-2	Sequence 2, App1
6	739.8	34.5	2073	US-10-781-979-4	Sequence 4, App1
7	172.4	8.0	3471	US-10-099-285-71	Sequence 71, App1
8	162.8	7.6	2407	US-10-428-285-71	Sequence 29, App1
9	133.6	6.2	4391	US-10-929-761-4	Sequence 5, App1
10	119.8	5.6	1959	US-10-428-361-5	Sequence 5, App1
11	117.6	5.5	1806	US-10-782-020-4	Sequence 2, App1
12	117.6	5.5	1890	US-10-782-020-2	Sequence 2, App1
13	117.6	5.5	2190	US-10-782-020-1	Sequence 1, App1
14	116.8	5.4	3684	US-10-428-961-62	Sequence 62, App1
15	113.4	5.3	2019	US-10-665-460A-7	Sequence 7, App1
16	112.4	5.2	3687	US-10-614-524-1	Sequence 1, App1
17	112.4	5.2	4173	US-10-428-961-37	Sequence 3, App1
18	111.8	5.2	2019	US-10-665-460A-1	Sequence 1, App1
19	111.8	5.2	2019	US-10-665-460A-3	Sequence 3, App1
20	111.8	5.2	3471	US-10-099-285-73	Sequence 27, App1
21	111.8	5.2	3471	US-10-428-961-27	Sequence 4, App1
22	111.8	5.2	4344	US-10-687-879A-4	Sequence 2, App1
23	110.8	5.2	1561	US-10-687-879A-2	Sequence 2, App1

24	110.2	5.1	2019	US-10-665-460A-5	Sequence 5, App1
25	105.4	4.9	2019	US-10-665-460A-11	Sequence 11, App1
26	105	4.9	1860	US-10-032-717-19	Sequence 19, App1
27	105	4.9	1860	US-10-414-637-19	Sequence 15, App1
28	105	4.9	1860	US-10-606-320-15	Sequence 15, App1
29	105	4.9	1860	US-10-746-914-15	Sequence 15, App1
30	105	4.9	2003	US-10-032-717-5	Sequence 5, App1
31	105	4.9	2003	US-10-414-637-5	Sequence 5, App1
32	105	4.9	2010	US-10-032-717-15	Sequence 15, App1
33	105	4.9	2010	US-10-414-637-15	Sequence 15, App1
34	105	4.9	2010	US-10-606-320-11	Sequence 11, App1
35	105	4.9	2010	US-10-746-914-11	Sequence 11, App1
36	105	4.9	3621	US-10-032-717-1	Sequence 1, App1
37	105	4.9	3621	US-10-414-637-1	Sequence 1, App1
38	105	4.9	3621	US-10-606-320-1	Sequence 1, App1
39	105	4.9	3621	US-10-746-914-1	Sequence 1, App1
40	105	4.9	3621	US-11-021-115-5	Sequence 5, App1
41	105	4.9	4874	US-10-032-717-27	Sequence 27, App1
42	105	4.9	4874	US-10-414-637-27	Sequence 27, App1
43	105	4.9	4874	US-10-606-320-17	Sequence 17, App1
44	105	4.9	4874	US-10-746-914-17	Sequence 17, App1
45	104.4	4.9	3687	US-10-809-953-9	Sequence 9, App1

ALIGNMENTS

RESULT 1
US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXM1-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-141-1

Query Match 100.0%; Score 2145; DB 8; Length 2145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTTCCACCAATATATATGTTTTTTTGTAGAAACATTTGTTCAGGAATATACATTGGGTACTA	60
DB	1	TTTCCACCAATATATATGTTTTTTTGTAGAAACATTTGTTCAGGAATATACATTGGGTACTA	60
QY	61	CGAATATATAGAAAGACACCTGGCATATATTTATTTAGTGTCTTAAATATAGACTATA	120
DB	61	CGAATATATAGAAAGACACCTGGCATATATTTATTTAGTGTCTTAAATATAGACTATA	120
QY	121	TAAAGAGTAAATATATGATTTCTTATCAAAATACAAATGAATATATATTCGATGCT	180
DB	121	TAAAGAGTAAATATATGATTTCTTATCAAAATACAAATGAATATATATTCGATGCT	180
QY	181	TTCCCGAATATACCAATATATGTCACAAAGATATCTTTTTCGAAAGATCCAAATATATTT	240
DB	181	TTCCCGAATATACCAATATATGTCACAAAGATATCTTTTTCGAAAGATCCAAATATATTT	240
QY	241	CCATTATTAACCTGAGCGCTTGTCAGGAGGCCATGGCAAGATATCGTGGAAATCATGCTCG	300

Db 241 CCTATTAACTGGACGCTTGTGACGGGAAGCCATGGCAATGACGTGGGAATCAAGCTCG 300
Qy 301 GATATAGTACTTATGGGACATACCTTATACAAATCTTGTGTAAGACCCGGTATAGGTGA 360
Db 301 GATATAGTACTTATGGGACATACCTTATACAAATCTTGTGTAAGACCCGGTATAGGTGA 360
Qy 361 ATTCCGTAATATTTTCAATATATAAACAATCCATTCGGTCTTGTGTAATCTGTGGCA 420
Db 361 ATTCCGTAATATTTTCAATATATAAACAATCCATTCGGTCTTGTGTAATCTGTGGCA 420
Qy 421 GCACTTTCTATATGTGATTTAGTATCTATATTTCTGTAAGAGGTAGACGAGCGTGTAA 480
Db 421 GCACTTTCTATATGTGATTTAGTATCTATATTTCTGTAAGAGGTAGACGAGCGTGTAA 480
Qy 481 AGTACGCGGGGTGCAAGATTTTGAAGGTGAATGACGTCTTATCAAGATTAATTTATCTTCAT 540
Db 481 AGTACGCGGGGTGCAAGATTTTGAAGGTGAATGACGTCTTATCAAGATTAATTTATCTTCAT 540
Qy 541 TATCTTGAAGATTTGCTTACAGATTAATCAATCTCTAAAAAACTTGTGCAAGTATTA 600
Db 541 TATCTTGAAGATTTGCTTACAGATTAATCAATCTCTAAAAAACTTGTGCAAGTATTA 600
Qy 601 CAGTCCCAAGCAGCGGGAAGAAATTTCACTAAACTTTTACAGGGTCAATATCAAGCAG 660
Db 601 CAGTCCCAAGCAGCGGGAAGAAATTTCACTAAACTTTTACAGGGTCAATATCAAGCAG 660
Qy 661 AAAGCTGAATATTTATTTATTTGCTTACAGTATGTCAGAGTCAAGTATTTATTA 720
Db 661 AAAGCTGAATATTTATTTATTTGCTTACAGTATGTCAGAGTCAAGTATTTATTA 720
Qy 721 TTAAGGGAAGCAGTAAATATTAATAAAGAAATGGGGAATAGTGTGTCCACCGTGTATCA 780
Db 721 TTAAGGGAAGCAGTAAATATTAATAAAGAAATGGGGAATAGTGTGTCCACCGTGTATCA 780
Qy 781 GGGTCAAGGGAAGCTGATTTGTAACGAGCGGTAAACCGAATAAAGATTAATTAAT 840
Db 781 GGGTCAAGGGAAGCTGATTTGTAACGAGCGGTAAACCGAATAAAGATTAATTAAT 840
Qy 841 TATTTGCTAGGGTGTATTAACAAGGTTTATGATCAATGAACAAGCGGGTATCAAGTGT 900
Db 841 TATTTGCTAGGGTGTATTAACAAGGTTTATGATCAATGAACAAGCGGGTATCAAGTGT 900
Qy 901 GAAGTTTGTGCAAAATTTAATAATTTCTGTAAGAAATGAAGTGGCGGTATTAATTAAT 960
Db 901 GAAGTTTGTGCAAAATTTAATAATTTCTGTAAGAAATGAAGTGGCGGTATTAATTAAT 960
Qy 961 ATTGCTATATTTTCAACTTATGATTTTGAATAATATTCATTAAGCAACAAGTATGA 1020
Db 961 ATTGCTATATTTTCAACTTATGATTTTGAATAATATTCATTAAGCAACAAGTATGA 1020
Qy 1021 ACTAGGGAATTTTATACAGATCCAGTGGGATTTTCAAGGGGGAATTTTGTGGGAACGG 1080
Db 1021 ACTAGGGAATTTTATACAGATCCAGTGGGATTTTCAAGGGGGAATTTTGTGGGAACGG 1080
Qy 1081 TTTTGTAGCTTAAATTCGTAGAAAGCAATGGAACAGCGGGGACCTGGTTATAGTAACTGG 1140
Db 1081 TTTTGTAGCTTAAATTCGTAGAAAGCAATGGAACAGCGGGGACCTGGTTATAGTAACTGG 1140
Qy 1141 CTTCAAGCTATAGATATATATAGTCAATTAATCTTCAAGCTTGTATCTTATAGTGC 1200
Db 1141 CTTCAAGCTATAGATATATATAGTCAATTAATCTTCAAGCTTGTATCTTATAGTGC 1200
Qy 1201 TGGGGGGGAAGCTGTCTATATGAAGACTTCAACAAGGGTAAACGGTGTCTTTCAACGTATG 1260
Db 1201 TGGGGGGGAAGCTGTCTATATGAAGACTTCAACAAGGGTAAACGGTGTCTTTCAACGTATG 1260
Qy 1261 TCTGAAGCTAGATATATATCCAGTATATTTTGTGGCAATACCGATATATTTAA 1320
Db 1261 TCTGAAGCTAGATATATATCCAGTATATTTTGTGGCAATACCGATATATTTAA 1320
Qy 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGTATTTCAATCCACGGCAT 1380
Db 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGTATTTCAATCCACGGCAT 1380

Db 1321 ATTATTTCAATAGCTAGATATGCAATCAACCGTTGTGGTATTTCAATCCACGGCAT 1380
Qy 1381 CTTGTTTCAAGTGAAGATTTTTCGACACACTTAATCTTCTGTATATAGGTAAAC 1440
Db 1381 CTTGTTTCAAGTGAAGATTTTTCGACACACTTAATCTTCTGTATATAGGTAAAC 1440
Qy 1441 AGTTGGGATCTACAGACAAATTTGATCTGTATACAGAGTATTAATTAAGATCTACCA 1500
Db 1441 AGTTGGGATCTACAGACAAATTTGATCTGTATACAGAGTATTAATTAAGATCTACCA 1500
Qy 1501 CCTAGCTGTAACAATTTACTCTCATGATATTAATCAATGCGGACGTCTCAAAATGAAC 1560
Db 1501 CCTAGCTGTAACAATTTACTCTCATGATATTAATCAATGCGGACGTCTCAAAATGAAC 1560
Qy 1561 TCCAGAGTAAAGTATTTGTTGGAACATTAACAATTAAGAAAAAGATTAATGAATTTAT 1620
Db 1561 TCCAGAGTAAAGTATTTGTTGGAACATTAACAATTAAGAAAAAGATTAATGAATTTAT 1620
Qy 1621 CCAGATTAATTAACCAATTTCTGCAATGAATTAAGCTTTTCCCTACAGAGTACAGGA 1680
Db 1621 CCAGATTAATTAACCAATTTCTGCAATGAATTAAGCTTTTCCCTACAGAGTACAGGA 1680
Qy 1681 TATGACAGAGTTCAGTCAACAGCTGGCTGTATTAACAAGAGAGATGTATTAACGTTA 1740
Db 1681 TATGACAGAGTTCAGTCAACAGCTGGCTGTATTAACAAGAGAGATGTATTAACGTTA 1740
Qy 1741 CCTTATCAAGCAAGTTTAAATATAGTTTAACTTGTGACCCACGAATTAATTAACGT 1800
Db 1741 CCTTATCAAGCAAGTTTAAATATAGTTTAACTTGTGACCCACGAATTAATTAACGT 1800
Qy 1801 GTTAGACTTCGCTACGCGAGTGAAGAACTGTCCGTCCGAGTGAAGAAAGATGTGCGCA 1860
Db 1801 GTTAGACTTCGCTACGCGAGTGAAGAACTGTCCGTCCGAGTGAAGAAAGATGTGCGCA 1860
Qy 1861 AGTCTGTTTCAAAATGCTAATTTTCTGTCAGGCTACAGGTGGCTATATAGTTCAAT 1920
Db 1861 AGTCTGTTTCAAAATGCTAATTTTCTGTCAGGCTACAGGTGGCTATATAGTTCAAT 1920
Qy 1921 TATGTCGACACTTGTATCTTATTAATTAATCAATGAGTGTGAATTAATTAATTA 1980
Db 1921 TATGTCGACACTTGTATCTTATTAATTAATCAATGAGTGTGAATTAATTAATTA 1980
Qy 1981 CTATCTGTTTCAACTTATTTGTTGAACAAGTGAATTTATCCCAATGACATCCAAAT 2040
Db 1981 CTATCTGTTTCAACTTATTTGTTGAACAAGTGAATTTATCCCAATGACATCCAAAT 2040
Qy 2041 GAAAAATGTACGAATGTCAATTTGAAGAGACATATGTAGTGTGAAGAGTACATCC 2100
Db 2041 GAAAAATGTACGAATGTCAATTTGAAGAGACATATGTAGTGTGAAGAGTACATCC 2100
Qy 2101 TTGGAAACAAAAAAGATTTGTAAATAGTTTATTAATCAATTA 2145
Db 2101 TTGGAAACAAAAAAGATTTGTAAATAGTTTATTAATCAATTA 2145

RESULT 2
US-10-782-141-2
; Sequence 2, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Michael B.
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR APPLICATION NUMBER: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-10-782-141-2

Query Match      94.1%; Score 2019; DB 8; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      127 GTGAAAAATATGAAATCTTATCAAAATPACAAATGAAATGAAATTCGATGGTCCCG 186
Db      1 GTGAAAAATATGAAATCTTATCAAAATPACAAATGAAATGAAATTCGATGGTCCCG 60

QY      187 AATPACCAAAATATGTAATCTTATCCTTTGCAAGATCCAAATATATTTCTATTT 246
Db      61 AATPACCAAAATATGTAATCTTATCCTTTGCAAGATCCAAATATATTTCTATTT 120

QY      247 AACCTGACGCTTGTCAAGGAGCCATGGCAAGATACGTGGGAATCAGTCTGGATATA 306
Db      121 AACCTGACGCTTGTCAAGGAGCCATGGCAAGATACGTGGGAATCAGTCTGGATATA 180

QY      307 GTAACTATTTGGGACATACCTTATACAAATTCCTGTAAGACCCGGTATAGGTGAAATCT 366
Db      181 GTAACTATTTGGGACATACCTTATACAAATTCCTGTAAGACCCGGTATAGGTGAAATCT 240

QY      367 GTAAATTTTCAATTAATTAACAAATCTATCCGCTTCTGTGATCAATCTGAGCACTT 426
Db      241 GTAAATTTTCAATTAATTAACAAATCTATCCGCTTCTGTGATCAATCTGAGCACTT 300

QY      427 TCAATATGATTTAGTATCTATTAATCTGTAAGAGGTAGACGAGACGCTTAAGTAC 486
Db      301 TCAATATGATTTAGTATCTATTAATCTGTAAGAGGTAGACGAGACGCTTAAGTAC 360

QY      487 GGGGTTGCAATTTTGAAGGTGAAATGATCTGCTTATCAAGATTAATTAATCTTCAATTA 546
Db      361 GGGGTTGCAATTTTGAAGGTGAAATGATCTGCTTATCAAGATTAATTAATCTTCAATTA 420

QY      547 GAGATTTGGCTTACAGATAATCAATCTTAAAAAATTTGCTGACGTAAGTAAACAGTTC 606
Db      421 GAGATTTGGCTTACAGATAATCAATCTTAAAAAATTTGCTGACGTAAGTAAACAGTTC 480

QY      607 CAAGCAGGGAAGAAATTCATTAACCTTTAGCAGAGTCAATTAACAGAGAAAGCT 666
Db      481 CAAGCAGGGAAGAAATTCATTAACCTTTAGCAGAGTCAATTAACAGAGAAAGCT 540

QY      667 GAAATATTAATTAATGCTTACGTAAGTCAAGCTGCAAAATGCAATTTATTAATTAAG 726
Db      541 GAAATATTAATTAATGCTTACGTAAGTCAAGCTGCAAAATGCAATTTATTAATTAAG 600

QY      727 GAGCAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 786
Db      601 GAGCAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 660

QY      787 GGGAGAATCTAATTTGTAACGAGCGTTTAAAGCGAAAAATTAAGAGTATCTAATTTATTT 846
Db      661 GGGAGAATCTAATTTGTAACGAGCGTTTAAAGCGAAAAATTAAGAGTATCTAATTTATTT 720

QY      847 GTAGGTTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTACAAAGTCTGAAGT 906
Db      721 GTAGGTTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTACAAAGTCTGAAGT 780

QY      907 TGATCGAAATTTTAATTAATTTTGTGAGAGAAATGACCTTGGCGGTATGATATTAATTTGCT 966
Db      781 TGATCGAAATTTTAATTAATTTTGTGAGAGAAATGACCTTGGCGGTATGATATTAATTTGCT 840

QY      967 ATAATTTCAACTTATGATTTTGAAGAAATATCAATTAAGCAAGAGTGAAGTAACTAGG 1026
Db      841 ATAATTTCAACTTATGATTTTGAAGAAATATCAATTAAGCAAGAGTGAAGTAACTAGG 900
```

```
QY      1027 GAAATTTATACAGATCCAGTGGAGATTCAGGGGAAATTAATGATGGGAAACGGTTTTTT 1086
Db      901 GAAATTTATACAGATCCAGTGGAGATTCAGGGGAAATTAATGATGGGAAACGGTTTTTT 960

QY      1087 AGCTTTAATTCGGTAAAGCAATGGAACACCGGGGACCTGGTTTATGTTACTTGGCTTCAA 1146
Db      961 AGCTTTAATTCGGTAAAGCAATGGAACACCGGGGACCTGGTTTATGTTACTTGGCTTCAA 1020

QY      1147 GCTATAGATATATATAGTCAATCTTATTAATCTTCAAGCTTGGTATCTTATGCTGGGG 1206
Db      1021 GCTATAGATATATATAGTCAATCTTATTAATCTTCAAGCTTGGTATCTTATGCTGGGG 1080

QY      1207 GGAATCTGCTATTATGAGACCTTACAAAGGGTAAACGGTCTTTCAACCTATGCTGGA 1266
Db      1081 GGAATCTGCTATTATGAGACCTTACAAAGGGTAAACGGTCTTTCAACCTATGCTGGA 1140

QY      1267 ACTACGAGTAAATATCAAGTATATTTATTTTGGCAATACGATATATTTAAATTAAT 1326
Db      1141 ACTACGAGTAAATATCAAGTATATTTATTTTGGCAATACGATATATTTAAATTAAT 1200

QY      1327 TCAATTAAGTATGATGAAATGCAACCGTTTGTGGGATTCATCCCAAGGCACTTGT 1386
Db      1201 TCAATTAAGTATGATGAAATGCAACCGTTTGTGGGATTCATCCCAAGGCACTTGT 1260

QY      1387 TCACTGCAAGAAATTTTTCGACAAACATAATCTTCTGTATAGAGTAAACAGTTCT 1446
Db      1261 TCACTGCAAGAAATTTTTCGACAAACATAATCTTCTGTATAGAGTAAACAGTTCT 1320

QY      1447 GGGTACTCAGACACATTTGAATCTGTGTTACAGGTTTAAATAGATCTTACCACTAGT 1506
Db      1321 GGGTACTCAGACACATTTGAATCTGTGTTACAGGTTTAAATAGATCTTACCACTAGT 1380

QY      1507 CGTACAAATTAATCTCTATAGATTAATCAAAATGCGGCAATGTTCAAAATGAACCTCCGA 1566
Db      1381 CGTACAAATTAATCTCTATAGATTAATCAAAATGCGGCAATGTTCAAAATGAACCTCCGA 1440

QY      1567 GTTAACGATTTTGGTGAACATACAGATGATGAAAAAGATATGAAATTTATCCAGAT 1626
Db      1441 GTTAACGATTTTGGTGAACATACAGATGATGAAAAAGATATGAAATTTATCCAGAT 1500

QY      1627 AAAATTAACGAAATTTCTGCAAGTAAAGCTTTTCCCTACAGAGGTACAGATATGCA 1686
Db      1501 AAAATTAACGAAATTTCTGCAAGTAAAGCTTTTCCCTACAGAGGTACAGATATGCA 1560

QY      1687 GAGGTTACGTCACAGCTGGGCTGTTTATACAGAGAGATGTAGTAACGTAACCTAT 1746
Db      1561 GAGGTTACGTCACAGCTGGGCTGTTTATACAGAGAGATGTAGTAACGTAACCTAT 1620

QY      1747 CAAGCAAGTTTAAATAAGTAACTTGTACACCCACGAAATTAATTAACCGTGTAGA 1806
Db      1621 CAAGCAAGTTTAAATAAGTAACTTGTGTACACCCACGAAATTAATTAACCGTGTAGA 1680

QY      1807 CTTGCGTACGCGAGTGAAGACCTGGTCCGTTCCGATGAAAGATGCTGCCAAGTTCT 1866
Db      1681 CTTGCGTACGCGAGTGAAGACCTGGTCCGTTCCGATGAAAGATGCTGCCAAGTTCT 1740

QY      1867 GTTTCAAAATGCTAATTTTCTGTCAGAGTAAAGAGGCTATGCTCAATTTGATTAATG 1926
Db      1741 GTTTCAAAATGCTAATTTTCTGTCAGAGTAAAGAGGCTATGCTCAATTTGATTAATG 1800

QY      1927 GACACCTTAGTATCTAATTAATCAATCAAGTGTGAATTAATTAATTAATTAATTAATCT 1986
Db      1801 GACACCTTAGTATCTAATTAATCAATCAAGTGTGAATTAATTAATTAATTAATTAATCT 1860

QY      1987 GGTACCACTTATTTGTGACAAAGTCAATTTATCCCAATTAATCAATTTGAAAAA 2046
Db      1861 GGTACCACTTATTTGTGACAAAGTCAATTTATCCCAATTAATCAATTTGAAAAA 1920

QY      2047 TGTACAAATGCTCAATTTGAGAGACATATGATGATGAAAGATACATCTTTGAA 2106
Db      1921 TGTACAAATGCTCAATTTGAGAGACATATGATGATGAAAGATACATCTTTGAA 1980
```


Db 1621 TTTAAATTAAGCTTTAACTTTCGACCCACCAATTAATTAACGCTTTAGACTTCGCTAC 1680
Qy 1816 GCGAGTGGAGAGCTGGTCCGTTCCAGTAAAGAAAGATGTCGCCAAGTTCGTTCAAT 1875
Db 1681 GCGAGTGGAGAGCTGGTCCGTTCCAGTAAAGATGTCGCCAAGTTCGTTCAAT 1740
Qy 1876 GCTAATTTTCTCGTCCAGCTACAGGTCGCTATGTTGATTTGATTTGAGACCTTA 1935
Db 1741 GCTAATTTTCTCGTCCAGCTACAGGTCGCTATGTTGATTTGATTTGAGACCTTA 1800
Qy 1936 GTTACTCATTTATATCAATGAGGTCGTAATATATTAACAAATCTATCGTTACAC 1995
Db 1801 GTTACTCATTTATATCAATGAGGTCGTAATATATTAACAAATCTATCGTTACAC 1860
Qy 1996 CTATTTGTTGCAAGAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACAAA 2055
Db 1861 CTATTTGTTGCAAGAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACAAA 1920
Qy 2056 TGTCAATTCGAGAGACATATGTATGTGAGAGAGTCAATCTTGAAACAAAAA 2115
Db 1921 TGTCAATTCGAGAGACATATGTATGTGAGAGAGTCAATCTTGAAACAAAAA 1980
Qy 2116 GAGATTGTAATATGTTATTTATTAATTA 2145
Db 1981 GAGATTGTAATATGTTATTTATTAATTA 2010

RESULT 4

US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Harzels, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-008, A Delica-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-781-979-1

Query Match 39.9%; Score 855; DB 8; Length 5980;
Best Local Similarity 71.4%; Pred. No. 3e-185;
Matches 125; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

Qy 8 AAATATATATTTTGTAGAAAACATTGTTACAGAAATACATTGGGCTACTAGAAAT 67
Db 49 AAATATATGTTATTTGTAGAAAACATTGTTACAGAAATACATTGGGCTACTAGAAAT 108
Qy 68 ATGAAAAGACACCTGGCATATATTTATTTAGGTGCTTTAAATTAAGACTATTAAGAG 127
Db 109 ATGAAAAGACACCTGAATATATTTATTTAGGTGCTTTAAATTAAGACTATTAAGAG 168
Qy 128 TGAATAATATGATTTCTTATCAAAATCAATGAATTAAGAAATTCGAAAGTTCCTCCGA 187
Db 169 TGAATAATATGATTTCTTATCAAAATCAATGAATTAAGAAATTCGAAATTCCTCCGA 228
Qy 188 ATTAACAATAATATGTTCAAAAGATATCTTTTGCAGAAAGATCCAAATATATTTCTATTA 247
Db 229 ATTAACAATAATGCGCCAAAGATATCTTTTGCAGAAATATTCGAGATATATCTATATGT 288

Qy 248 ACCTGACGCTTGTGACGGAAGGCCATGCGAAGATACGTGGAAATCACTCGGATATAG 307
Db 289 CTGGAAATGATTTCTGAGGAAATCTCATGGATGATAAATTTGGAAATCGTGAAACGATTA 348
Qy 308 TAACATATGGGACATACCTTATCAAAATCTTGTGAGAACCCGGTATAGTGAATTCCTG 367
Db 349 CAAGTATTTGGGATTAATCTTATAGAGTTGTGTATAGAACCTTATGTTGGTGAATTAATA 408
Qy 368 TAATATTTTCAATTAATTAACAAACCTCATTCGTCCTTGTGCAATCTTGACGACCTTT 427
Db 409 CACTATTTATCAATTAATTAAGAAAACCTAATTCGACTAATGCTCAACCTGTGACACCTTT 468
Qy 428 CTATATGATTTATGATTTCTATTAATTCGTAAGAGGTGAGACGAGCGTGTAAATAGTACG 487
Db 469 CTATATGATTTATGATTTCTATTAATTCGTAAGAGGTGAGACGAGTGTAAATAGTACG 528
Qy 488 GGGTGCAGATTTTGGAGGGAATGACCTGCTATCAAGATTAATTAATCTTCAATATCTTG 547
Db 529 CGATTCGAGATTTTGCAGGTAATTAATTAAGAAATTTATAGAGATTTATCTTTCTATCTTG 588
Qy 548 AGGATTTGGCTTACAG-----ATAATCAATCCTAATAAACTTGCTGACG 592
Db 589 GGGCTTGGCTTAAAGACGTAACCACTTCAAAAAGCAATTAATTCGATATGACAAAT 648
Qy 593 TAGTTAAACGTTCCAGACCGGAAAGAGATTTCACTAACTTTTACGCGGCTATAT 652
Db 649 TAGTTATTAATTTTAAACCTTTCAGAAAGAGATTTCAATGAATTTCTAGAGGGGTCAATGT 708
Qy 653 CAAGACAGAAAGCTGAATTTATTTATGCTGCTAGTATGACAGGCGCAATGTCATT 712
Db 709 CAAGAAACAAATGCTCAAGTATTTTATTTACCTTATGACAGGCTGCAAAATGTCAGT 768
Qy 713 TATTACTATTAAGGAGCGCATTAATTAATTAAGAAAGATGGGACTAGTGTCCACCGT 772
Db 769 TATTACTATTAAGGAGTGAAGTCAATTAATTAAGCAAGATGTTCCATTTTGAATGACG 828
Qy 773 TGTATCAAGGCTGACGAGAA-----CTGATTTGTA 802
Db 829 AGAATGTAGATGCGAATTAATTAATTAATCACTAACAGTGTGTGATTTTACCGGTAATTA 888
Qy 803 ACAGAGGGTTAAAGGAAATAAAGAGATTAATTAATTTGAGAGGGTGAATTAACA 862
Db 889 ATAGAGGATTTAAATGCAAAACGAGAGATTAATTAATTTGATTTGATTTGATTTGATTTG 948
Qy 863 AGGTTTATGATGATTAAGACAGCGCGGTACAGTCTGAGTGTGTCGAAATTTAATA 922
Db 949 TAGTTTAAATGATTAAGAAACAGCGGGGACAGTGTCTGCACTTGGTGCAGAAATTTAATA 1008
Qy 923 AATTTCGTAGAAATGACGTTGGCGGTATGGAATTAATTTGCTATATTTCAACTTAATG 982
Db 1009 AATTTCGTAGAAATGACGTTGGCGGTATGGAATTAATTTGCTATATTTCCAACTTAATG 1068
Qy 983 AATTGAAAATATTCATTAAGCAACAGGTGTAGATTAATTAATTAATTAATTAATTAATTA 1042
Db 1069 AATTGAAAATATTCATTAAGCAACAGGTGTAGATTAATTAATTAATTAATTAATTAATTA 1128
Qy 1043 CAGTGGGATTAATTCAGGCGGGAATTAATGTTGGAGCGGTTT-----TTAGCTTTAAT 1096
Db 1129 CAGTGGGATTAATTCAGGGAACCTTAATGTTGTTAGGAATTTGGCCTAATTAATTTAATG 1188
Qy 1097 CGGTAGAGCAATTAAGCAACGCGGACCTGTTTATGTTACTTGGCTTCAAGCTAATGATA 1156
Db 1189 GGTTAAGGCTAATTAAGCAACGCGGACCTGTTTATGTTACTTGGCTTCAAGCAATTAATGATA 1248
Qy 1157 TATATGCTATCTATTAATTTCACTGCTGTTATCTGATGTTGGCTGGGGGGAATCTGCT 1216
Db 1249 TATATATGATTAATTT-----TCGAGATATTTTGGCGCTGGTGAAGATCTGCT 1299
Qy 1217 ATTAATGAAGCTTCAAAAGGTTAAGGTCCTTTTCAAGCTATGTCGAACTAAGAGTA 1276
Db 1300 ATTAATGAAGCTTCAAAAGGTTAAGGTCCTTTTCAAGCTATGTCGAACTAAGAGTA 1359
Qy 1277 ATTAATCAAGTAAATTAATTTTGGCAATTAAGCAATTAATTTAATTAATTTCAATTAAGCTA 1336

Db 1360 ATGATCTAGCTATATGATTTTCAGAAATGCCAGATGATATTAATAATTACTCTATTAGCTA 1419
QY 1337 GATATGCAATGCAACCGTTTGTGGTATTCATCCACGGCATCTTGTTCACGTGCAG 1396
Db 1420 ---TCATGAACCTAGTAGAGACATACCGCTAGACAGATATCGTGTTCAAAGGCAG 1476
QY 1397 AATTTTTCGACACACCTAATAATCTTCTGTATAGAGTAACAGTCTGGG---TACT 1453
Db 1477 ATTTTGTAGGGTAGGGGGACCTGATTTTAATATATGACAGGTAATTAATGGCTAAGCA 1536
QY 1454 CACAGCAATTTGATCTGTGTACACAGTATTAATAGATCTACACACTAGTGTACAA 1513
Db 1537 GATGACAAATTTGATCTAGCTTCCACTGTATTTGACCTAA-----TGTGTAGAG 1590
QY 1514 ATTACTCTCTAATATTTCAATAGCGGACATGTGTTCAAAATGAACCTCCAGTTAAG 1573
Db 1591 GACCTCTCATATATATCAATAGCGGACATGTGTATATGGAATCTCCAGAGTTAAG 1650
QY 1574 TATTTGGTTGGACACATACAAATGATGAAAAAGATATGAAATTTATCCAGATAAATTA 1633
Db 1651 TATATGTTTGGACATACAAAGTTTAAACGTGAAATATATTTGAACCAATCAATTA 1710
QY 1634 CGCAATTTCTGACGTAAAAAGCTTTTGCCCTACACAGGATACAGATATGACAGAGTT 1693
Db 1711 CACAAATACCGGGGGTAGAGATTATTAATCTTCAAAATTTATCTGTAAATGCTATACCT 1770
QY 1694 AGCTCACAGCTGGGCT 1710
Db 1771 ATGTAATTAAGGCACT 1787

RESULT 5

US-10-781-979-2
; Sequence 2, Application US/10781979
; Publication No. US2004025031A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Harzels, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2082)
US-10-781-979-2

Query Match 34.8%; Score 747.2; DB 8; Length 2082;
Best local Similarity 69.8%; Pred. No. 9,9e-161;
Matches 1143; Conservative 0; Mismatches 433; Indels 72; Gaps 7;
QY 127 GTGAAAAATATGATTTCTTATCAAAATGAAATGAAATGAAATTTCTGATGTTCCCG 186
Db 1 GTGAAAAAGATGATCATATCAAAATTAATGAATATGAATATATGAAATCTCATCG 60
QY 187 AATTAACCAATATATGTAACAGATATCTTTTGCAGAAAGATCCAAATATATTTCTAT 246
Db 61 AATTAACCAATATGCGCAACAGATATCTTTTGCAGAAATATGCGGATATATGTCATATG 120
QY 247 AACTGACGCTTGTCAAGGAAGGCATGCAAGATAGTGGGAATCAGTCTGGAATATA 306

Db 121 TCTTGGAATGATGTCAGGGAATCTCATGGATGGAATTTGGGATTCAGTGAACGATA 180
QY 307 GTAATTTGGGACATACCTTATACATTTCTTGTAAGAACCGGATATAGTGAATTCCT 366
Db 181 ACAGATATTTGGGATTAATCTTATAGAGTTGTGATAGAACCTATAGTTGGGTGAATTAAT 240
QY 367 GTAATTTTTCATTAATAACAACTCATTCGCTTCGGGCATTCGTGGACACACT 426
Db 241 ACACTATATATCATATATGGAATACTAATTCGACTAATTCGCAACCTGTGCACACT 300
QY 427 TCTATATGATTTAGTATCTAATTTGTAAGAGATAGACAGAGCGGTATAGTAC 486
Db 301 TCTATATGATTTATTTATCTATATTTGTAAGAGATAGCGGATAGTATTTAAGTAT 360
QY 487 GGGGTTGCAGATTTGAGGGTGAATATGACTGTTATCAAGATTTATTTCTTATCTT 546
Db 361 GCGATTTGCAGATTTGACGGTAAATTTGAATAATTTAGAGATATTTATCTTTCTTATCT 420
QY 547 GAGSATTTGGCTACG-----ATAATCAAAATCCTAATAAACTTGCTGAC 591
Db 421 GGGGCTTGCTTAAAGACGTAACCACTTCAAAAGACAAATATTTGATATCGACAA 480
QY 592 GTAGTTAAACAGTTCCAGACGGAAGAATTTCACTAACTTTTACAGGTCATTA 651
Db 481 TTAGTTATTTATTTTAACTTTCAGAAAGATTTCAATGAATTTCTAGAGAGGTCAATTG 540
QY 652 TCAAGACAGAAAGCTGAATATTTATTTGCTTACGTATGTGCAAGCTGCAATGTGAT 711
Db 541 TCAAGAAACAAATGCTCAAGTATTTGTTATTTACTTCTTGTGCAAGAGCTGCAAAATGTG 600
QY 712 TTATTTACTTTAAGGAGCGCAGTAAATATTAATAAAGATGGGACCTGTGTGTCACCG 771
Db 601 TTATTTACTTTAAGGAGTACAGTTCAATTAATAAGCAAAATGTTCCATTTTGTAGTGA 660
QY 772 TTGTATCCAGGCTCAGGAGAA-----CTGATTTGT 801
Db 661 GGAATGTAGATTCGAATTAATATACCTAACAGTGTGTGATTTTACCGGTATTAAC 720
QY 802 AACGACCGTTTAAACGCAAAATTAAGATTAATTTATTTGTAGGGTGTATTAAC 861
Db 721 TATGACGATTTAAATGCAAAACGCGACAGTATACCAATTTATTTATTTATGATACG 780
QY 862 AAGGTTTATGATCAGTAAAGACAGCGGTAACAAGTGTGCAAGTTTGTGCAATTTAT 921
Db 781 GTATGTTTAAATCAGTAAACAGGCGGACAGGTGCTGACATTTGTGCAATTTAT 840
QY 922 AATTTCTAGAGAAATGACGTTGGCGGTATTTGATTTATTTGCTATATTTTCAACTAT 981
Db 841 AATTTCTAGAGAAATGACGTTGGCGGTATTTGATTTATTTGCTATATTTTCAACTAT 900
QY 982 GATTTGAAAAATATTCATTAGCAACAGTATGAGTATCTAGGGAATTTATACAGT 1041
Db 901 GATTTGAGAAATATTCATTAGCCAAACACATGTATGAGTTGACATAGGGAATTTATACAGT 960
QY 1042 CCAGTGGATTTTCAGGGGGAATTAATGTTGGGAACGGTTT-----TTAGCTTTAT 1095
Db 961 GCAGTGGATTTTCAGGGGCTTATAGTTGCTTACGAATTTGGCTTAATCTTTTAT 1020
QY 1096 TCGGTAGAGCAAAATGGAACACGCGGACCTGTTTATGTTACTTTGCTTCAACTATAGAT 1155
Db 1021 GGGTTAGAGCTTAATGGAACACGCGGACCTGTTTATGTTACTTTGCTTCAAAATAGAT 1080
QY 1156 AATATATGATCTTATTTATCTTCACTGTGTATCTTATGTCGTGGGGGGAACCTGCT 1215
Db 1081 AATATATATGATATGTT-----TCGATATATTTTCCGGGCTGGGTAGAACTCGT 1131
QY 1216 CATTAAGAGACTTCAAGAGGTAACGTTGCTTTTCAACGATGTGGAACCTACGAT 1275
Db 1132 CATTAAGAGACTTCAACAGGGAACGTTATTTTCAACGATGTGGAACCTACGAT 1191
QY 1276 AATTAATCCAGTAAATTTATTTTGGCAATACCGATATATTTAAATTTATTTATTTAGCT 1335

Db 1192 AATGATCTACGTAATATTGATTTTCAGAAATGCCATGTATATATAAATTACTTCATTAGCT 1251

Qy 1336 AGAATATGCAATATGCAACCGCTTTTGTGGGATTTCAATCCGACGGCATCTTGTTCACGTGCA 1395

Db 1252 A---TCATGAACCTAGTAGAGAGACCTACCGCTAGACACAGAGTATCGTGTTCGTTTCAAAAGCA 1308

Qy 1396 GAATTTTTTCCGACACACACTAAATACCTTTCTGTATGAGGTAAACAGTTCTGGG---TAC 1452

Db 1309 GATTTTCGTAGGGTAGGGGAGACCTGATTTTAATATATGATGACAGGTAAATATAGGGCTAAGC 1368

Qy 1453 TCACAGACAAATTGAATCTGTGTGTACAGGTATTAATGAATCTACACCTATGTGTGACA 1512

Db 1369 AGGATGACAATATGAATCTACGTTCCCACTGT-----ATTGACCTAAATGGTGTAGA 1422

Qy 1513 AATTACTCTCATTAATTTTCAAAATGGCGCATGTGTTCAAAATGAAACCTCCAGAGTTTAC 1572

Db 1423 GGACCCCTCTCATAGATTATTCAAAATGGCGCATGTGTGTATATGGAAATCCAGAGTTTAA 1482

Qy 1573 GTATTTTGTGGACACATACAAAGTATGAAAAAAGTATATGCAATTTATCCAGATTAATAAT 1632

Db 1483 GTATATGGTTTGGACACATACAAAGTTTAAAAAGTGAATAATATATGGAAGCCAAATCAATTT 1542

Qy 1633 ACGCAAAATTCGTGACGTAAAGCTTTTGCCCTACACAGAGTATACGATATGACGAGGT 1692

Db 1543 ACACAAAATACGGGGGTGAAGAGTTATTAACCTTCAAAATTAATCTTGTCTAATGGCTTAACC 1602

Qy 1693 TACGTCACAGCTGGGGCTT 1710

Db 1603 TATGTAAATAAAGGCACCT 1620

```

RESULT 6
US-10-781-979-4
; Sequence 4, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2073)
; US-10-781-979-4

```

Query Match	34.5%	Score 739.8	DB 8	Length 2073
Best Local Similarity	69.7%	Pred. No. 4.9e-159		
Matches 1135	Conservative 0	Mismatches 422	Indels 72	Gaps 7
Oy	136	ATGAATTTCTTATCAAAATACAAATGAATATGAAATTTCTGATGGTTCGCCGAATACACA	195	
Db	1	ATGAGTCATATCAAAATAAAAATGAATATGAAATATGAGATCTCTCATCAATACACA	60	
Oy	196	AATATGTCMAACAGATATCTTTTGCAAGAGATCCAAATATATTCTCATTAACCTGGAC	255	
Db	61	AATAGGCCAAACAGATATCTTTTGCAAAATTAATGGGATATGCTACTATATGCTTGGAAAT	120	
Oy	256	GCTTGTCCGGAAGGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATAGTAATTT	315	

D	b	121	GATTGTGACGGAACTCTGATGGGATGAATTTGGGAATCAGTCCGAAAGATACAGTAACAAGATT	180
O	y	316	GGGACATACCTTATACAAATCTTGTCTGAGAACCCGGTATAGGTGGAAATTCCTGTAAATTT	375
D	b	181	GGGATTAATCTTTATAGAGTTTGTGATAGAAACCTAGTTGGGTGGAAATTAATACATATTA	240
O	y	376	TCGATTAATTAACAACATCATTTCCCTCTTGTGTCAATCTGTGGAGCATTTTCTATATGT	435
D	b	241	TCGATTAATTAAGGAAACATTAATTCGACATTAATCGTCAAACTGTGTGACGACATTTCTATATGT	300
O	y	436	GATTAGATCTATTAATTCGTAAGAGGTGAGACGAGACGGTGAATGAACGGGGTTCGA	495
D	b	301	GATTATTAATCTATTAATTCGTAAGAGGTGAGACCGATAGTGTTTTAAGTATGATGCAATTCGA	360
O	y	496	GATTTTGAGGGTGAATGACTGCTTATCAAGATTATATCTTCAATATCTTGAGAGATTGG	555
D	b	361	GATTTTGACGGTAAATTTGAAAAATTAAGAGATTAATCTTCTTATCTTTGGGGCTTGG	420
O	y	556	CTTACAG-----ATAAATCAAATCTTAAAAAACTTGCTGACGTATGTTAA	600
D	b	421	CTTAAAGACGGTAAACCATTCGTAAGAAACAAATTAATCTGATATCGGACAAATTAGTTAT	480
O	y	601	CAGTTTCAAGACGGGAGAAAGATTTCACATTAACCTTTACAGAGTCAATATACAGACAG	660
D	b	481	TATTTTAACTTTCAGAAAGATTTCAAGAAATTCATAGAGAGGTCAATGTCAAGAAC	540
O	y	661	AAAGCTGAATAATATATATTATGCTCAAGTATGTGCAAGCTGCAAAATGTGCAATTTATCTA	720
D	b	541	AATGCTCAGATTTGTATTATTAATCTTACTTGTGCACAGCTGCAAAATGTGCAATTTATCTA	600
O	y	721	TTAAGGACGCGATTAATAATTAATAAAAGAAATGGGACATAGTGTGTCCACCGTGTATCA	780
D	b	601	TTAAGGATGCGATTCATATTAAGACACAATAGTGTCCATTTTGTGAGTGCAGAGAAATGTA	660
O	y	781	GGGTCAAGGAGAA-----CTGATTTGACGACGG	810
D	b	661	AGATCGGAATTTAAATATCACTTAACAGGTGTGTGATTTTACCGGTGATTTACTAAGACGA	720
O	y	811	TTAAAGCGAAAAATPAAGAGTATCAATTAATTTGTGTAGGGTGTATPAACAAGGGTTTA	870
D	b	721	TTAAATGCGAAACCGCAGATATACCAATTAATTTGTATTATATGTATACGATAGGTTTA	780
O	y	871	GATCAGATPAAGACAGCGGGGTACAAAGTGTGAAGTTTGTGAAATTTAAATAATTTCGT	930
D	b	781	AATCAGATPAACAAGGGGGGACAGGGTGCACACTGTGTGCAAAATTTAATAATTTCGT	840
O	y	931	AGAGAAATGACGTTGGCGGTATTTGATATTAATTCCTAATTTCCACTATGATTTGAA	990
D	b	841	AGAGAAATGACGTTGGCGGTATTTGATATTAATTCCTAATTTCCACTATGATTTGAG	900
O	y	991	AAATATCCATTAGCAACAAGTATGAGTTAACTAGAGAAATTTATACAGATCCAGTGGGA	1050
D	b	901	AAATATCCATTAGCCACAACAATGTAAGTTTAACTAGAGAAATTTATACAGATCCAGTGGGA	960
O	y	1051	TATTCAGGGGAAATTAATGTTGGGAAACGGTTTT-----TTAGCTTAAATCGGTAGAA	1104
D	b	961	TATTCATCGGGAACTTAATAGTTGGTTACGGAATTTGGCTTAATCTTTTAATGGGTTAGAG	1020
O	y	1105	GCAAAATGAAACAGCGGGACCTGTTAGTTACTTGGCTTCAAGCTATAGATATATATAGT	1164
D	b	1021	GCTAATGGAACACGGGAGACCTGGTTTGTACTTGGCTTAGCAAAATAGGATATATATAT	1080
O	y	1165	CATTCATTAATCTTCAGCTTGTGTATCTTAAGTGTGGGGGGGAATCGTCATATAGAA	1224
D	b	1081	GAGATATGT-----TCGAGATATTTTGGCCGGCTGGGTAGGAACTGTCAATTAAGAA	1131
O	y	1225	GACTTCACAAAAGGTAAACGGTGTCTTTCAACGATATGCTGGAACATCAAGATAATATCCA	1284
D	b	1132	GACTACACAAAGGTAAACGGTATTTTTCACAGTATGTCTGGAATCTAGATTAATATCTA	1191
O	y	1285	CGTAAATATATTTTGGCAATACCGATATATTTAAATTAATTTCAATTAAGCTATAGATATGA	1344
D	b	1192	CGTAAATATATTTTCAAGATGCGGATGTATTAATAATTAATTTCAATTAAGCTA---TCATG	1248

Sequence 29, Application US/10428961
Publication No. US2003023711A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chin-Rel
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rudar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
FILE REFERENCE: MECO201-1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/151,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
LENGTH: 2407
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-428-961-29

Query Match 7.6%; Score 162.8; DB 6; Length 2407;
Best Local Similarity 53.4%; Pred. No. 1.5e-26;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

QY 287 GGGAAATGAGTCTGGATATATGTAATCTATGGGACATACCTTATCAATCTCTGTAGAAC 346
DB 158 GCGATGACGAAAGAAAGCAATCTATATGGGACAAACATGCTCTCTATACACACAC 217
QY 347 CCGGTATAGTGTGAATCTCTATATATTTT-----CAATAATAACAAACCTATCCGT 400
DB 218 CTCTCTTACTGATTAATTTCAATATATAGTACCTTAATAGTAAGTCTAGAGAGTA 277
QY 401 CTCTGTGATCTGTGGACACTTCTATATGTATAGTATTAATTAATTCGTAAG 460
DB 278 GTATGTGACATCATATCAGATTTGTATATGTGACTTATTAATTAATTAATTAAT 337
QY 461 AGGATGACGAGGCTTAAAGTGAAGGCTTGAATTTTGAAGGCTGAATGACTCT 520
DB 338 GGGTAACTCAAGTGTATTAATGATGAGATGCAATTTAATGTTCTGACTCTTAT 397
QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAAGATTTGCTTACAGATA 565
DB 398 ACAGAACTATTTAGAGGCTGTGATAGTGAATTAAGATTCATTTCTGCTCTG 457
QY 566 AATCAATCTTAAAAAATTGCTGACGTAATTAACAGTTCAAGCAAGGAAAGAGATT 625
DB 458 AAGAACTCCGTACTCGTTTAAATCGCCGACTCAGAAATTTGAATTTTAAACCGAG 517
QY 626 TCACTAACTTTTACGAGGCTTATCAAGACAGAAAGTGAATTTTATTTGCTTA 685
DB 518 GGTCTTTTAAAGAAATGTGCTCTGTTAGTACAGCAAAATGCTCAATTTATTAATCTT 577
QY 686 CGTATGTGCAAGTGCATATGTCATTTATTAATTAAGGACGCAAGTAAATATATAA 745
DB 578 CTTTGTGAGCGCTGATTTTTCATTTATTAATTAAGGATGCTAGTATGATGCA 637
QY 746 AAGATGGGACATATGTGTTCACCGTTGATCCAGGCTCAAGGAAAGTATTTAGC 805
DB 638 CTAAATTTGGGGCTATACAAATGCTACACCTTTATTA-----ATTATCAAT 682
QY 806 AGCGTTTAAAGGAAATATAAGATTAATTAATTTAGTATGAGTGTGATTAACAG 885
DB 683 CAAATCTAGTACCTTATTTGAATTAATTAATTAATTTAGTATGAGTGTGATTAACAG 742
QY 866 GTTTAGTATGATTAAGACAGGCTGATCAAGTGTGATTAATTTAGTATGATTAATTAAT 925
DB 743 GTTCAACGAACTAAGACAGAGGCTGATGCTGATTAAGTGTGATTAATTTCAATGAT 802

QY 926 TTGCTAGAGAAATGACCTTGGCGGTATTTGATATTTATGCTATATTTTCAACTATGATT 985
DB 803 ATCGAGAGAGATGACATTTATGAGATTTAGAAATAGTACATCTTTTCAAGCTTGATA 862
QY 986 TTGAAATATTCATTTGACAAAGTGTAGATTTAATTAAGGAAATTTATACAGATCAG 1045
DB 863 TTACTAATTTACCAATTAAGAAAGATTTTATGATTTGATGAGTCAATTTATACAGATCAA 922
QY 1046 TGGGATATTCAGGGGAAATTAATGTTGGAA 1077
DB 923 TTGGTTTGTACATCTGATGATGCTTACGAGGA 954

RESULT 9
US-10-929-754-4
Sequence 4, Application US/10929754
Publication No. US20050124803A1
GENERAL INFORMATION:
APPLICANT: ABDULLAH, MOHD AMIR
APPLICANT: DEAN, DONALD H.
TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
FILE REFERENCE: 22727/04179
CURRENT APPLICATION NUMBER: US/10/929,754
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 4
LENGTH: 4391
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-929-754-4

Query Match 6.2%; Score 133.6; DB 9; Length 4391;
Best Local Similarity 48.1%; Pred. No. 1e-19;
Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;

QY 666 TGAATATTTATTTATGCTTATGCTATGTCAGAGTGCAGCAATGTCATTTATTAATTAAG 725
DB 1303 TGAGTTACTTTTATGCTCTCTATGACAAATTTGCAATCTGATTTACTTTATTAAG 1362
QY 726 GGAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 785
DB 1363 GGAATGCTAGATTTATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1407
QY 786 AGGAAATGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 845
DB 1408 TGCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1467
QY 846 TGTAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 905
DB 1468 TATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1516
QY 906 TTGCTGAAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 965
DB 1517 -TGGTAAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1575
QY 966 TATATTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1025
DB 1576 AATGTTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1635
QY 1026 GGAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1085
DB 1636 GGAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1692
QY 1086 TACCTTTAATTCGTATGAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1145
DB 1693 TTCTTTTGAAGAACTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1752
QY 1146 AGCTATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1205
DB 1753 AGGATTTCAATTTGTAACCAATTTCTATTTTATTTGACATTTTATTAATTAATTAATTAAT 1812

```
QY 1206 GGGAACTCGCATTATGAAGCTTCAAAAGGGTAACGGTCTTTCAAGTATGCTGG 1265
DB 1813 TAAAGTATCTTAACTAATATATCTAGTATTAACGAGGGCTCTTGGGGACAGAC 1872
QY 1266 AACTACGAGTAATATCAAGTAATATATTTT---GGCAATACGATATATTTAAAT 1322
DB 1873 AGATATNGTGGGACTTCTTCACTATATATTCATCAAAATTCGATCTATATAATTT 1932
QY 1323 TATTTCAATAGCTAGATATGCAATGCAACCGTTGTTGGTATCA---ATCCACGGCA 1379
DB 1933 ATGACGGAATAATATATATATATCTTGGGGGATCCGTAATATTTCAAAAAT 1992
QY 1380 TCTTGTTCACGTCGAATTTTTCGACACATTAATACCTTCTGATAGGTAA 1439
DB 1993 GAATTTTTCGTAAACGATATATATCTTCAAAAGATTAATATATGTCACACAGAC 2052
QY 1440 CAGTCTGGGTACTCAAGCAATGCAATCTGTTACAGTATTAATATAGATCTAC 1499
DB 2053 GATATAACCTGTTGTCGACAGATTTTGATTTTTCACATTAATAGAGAACTGAGTT 2112
QY 1500 ACTTACTGTCATAATTTACTCTATAGATTTCAATTCGGCATGTGTTCAAAA----- 1553
DB 2113 AGCAAAATATAAATGATATATATATCTTATCTATATGTTAATTAATGGGAAACGTT 2172
QY 1554 ---TGAACCTCGAGTAAAGTATTTGGTGGACACATACAGTATTAATAGAAATTA 1610
DB 2173 TGTTCGAAACGTCATGTTATTCGTTTCTTTACATATAGTATGATCTTAATTA 2232
QY 1611 TCGAATTTTTCAGATTAATTAATGCAAAATTCCTGCAATTAAGCTTTGCCCCACAG 1670
DB 2233 TACCATTTGACGAATTAATTAATGCAAAATTCCTGATAGTAAAGCTTCGATTAATAG 2292
QY 1671 AGGTACAGATATGCAAGAGGTATACGTACAGCTGGGCTGTTATACAGAGAGATGT 1730
DB 2293 ATGATTTTCAATGAAAAAGT-----CCCGAATTTACGGGAGAGATTT 2337
QY 1731 AGTACGTTACTTTATCAAGCAAGTTTAAATACGTTTAACTTTCGACCCACGAATTA 1790
DB 2338 GGTAAAGATGAGAGCAATTCAGGTTTAACTATGCGTTTAAAGCTGAATTTATAGTAA 2397
QY 1791 AAATTAACGTTAGACTTCTGCTACCGGAGTGAAGACCTGTCCTTCCGAGTAAAG 1850
DB 2398 AAATATCGTGTTCGATATAGTTATAATGTAACGTTCTAAATTAATATCTAGAAA 2457
QY 1851 ATGG---TGGCAAGTTCTGTTCAATGCTAATTTTCTGTCACGCTACAGGTGCTA 1907
DB 2458 ATGAAAAGGGAGGTTATATACAAACAAATTTCAAAATTTTCTCCCATATGAGAGC 2517
QY 1908 TAGTCATTTGATTTATGTCACACCTTATCTACATTTAATCAATCAGGTGTAAT 1967
DB 2518 CTTTCTTATTTAGAGCTTTTACTATATCTACAGCAAAATATATTTGATTTGACAA 2577
QY 1968 AATTAATACAAATCTATCTGTTACCACTTATTTGTCACAAAGTCGAATTTATCCAA 2027
DB 2578 GAGGTAAACATATCCGATGATGAGACGTTTGTGAAGATATACATCTCTATATATGA 2637
QY 2028 TGAATTCCAAATGAAAAATGTCGAATGTCAATTCGAAGAGACATATGATGATGA 2087
DB 2638 TAAATTCGAATTCCTCCCACTAATGATCAATTCACA-----GGAATATATGA 2686
QY 2088 AGGAGTACATCTCTGGAAACAAAAAGATTTGTAATAGTTTATTTCAATTA 2145
DB 2687 GGAATAATATGATATGAAAGATCACGAAACATTTAATATATTTGTTGATTA 2744
```

RESULT 10
US-10-428-961-5
; Sequence 5, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rel

```
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Ruper, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)  
CURRENT APPLICATION NUMBER: US/10/428,961  
PRIOR FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 1959  
TYPE: DNA  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-5
```

Query Match 5.6%; Score 119.8; DB 6; Length 1959;
Best Local Similarity 55.0%; Pred. No. 1e-16;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

```
QY 561 AGTAAATCAATCCATAAACTTGCAGCTAGTTAAACAGTCCAAAGCAGGAGAGA 620
DB 411 AGTAAACGAATATGATGCAAGATCAAGAGCATTTATCTTGAGCGCTATGCTTTAGA 470
QY 621 AGATTTACTTAACTTTTACAGGGTCAATTATCAAGACAGAAAGCTGAATATATAT 680
DB 471 ACTTGACATTTACTAGCTATACCGCTTTTCAAGATACGAATATGAAAGATTCATAT 530
QY 681 GCTACGATATGCAAGCTGCAAAATGATGATTTATTAATTAAGAGACGCTAAATA 740
DB 531 AATGATATATGCTCAAGCTGCAAAATTTACCTATATATATTAAGAGACGATCCCTTT 590
QY 741 TAAAAAAGATGGGACATAGTGTCCACCGTTGATCCAGGGTCAAGGAGATGATG 800
DB 591 TGGTATGATATGGGGATGAGCATCTTCGATTTTAAACAA-----TA 632
QY 801 TAACGACGGTTTAAAGCGAAATTAAGATATATTAATTTGTAGGGGTATTA 860
DB 633 TTACGAGAAACAATCAGATATACAGAGATATTTTAACTATGCGTACAAATGATTA 692
QY 861 CAAGGTTATGATCAGATTAAGCAGGCGGTACAGTGTGAAAGTTTGTGCAATTTA 920
DB 693 TACAGGGCTAAATTAATTAAGA-----GGGCAATGCTGAAGTGTGCGGTATTA 746
QY 921 TAAATTCGTAGAGAAATGACGTTGGCGGTATGATATATTTGCTATATTTCAACTTA 980
DB 747 TCAATTCGTAAGACCTTAAGTTAGGGGTATTAATTTAGTATGCTTATCCAAAGCTA 806
QY 981 TGAATTTGAAAAATATCCATAGCAACAGTATGAGTTAATTAAGAAATTTATACAGA 1040
DB 807 TGATATCCCATATATCCATCAATACGATGCTCAGTTAACAAGAAATTTATACAGA 866
QY 1041 TCAAGTGAATATTCAGGGGAAATTTATGTTGGGAACGTTTATAGCTTAA 1095
DB 867 TCAATTTGGAGAACAAATGACATTCAGATTTGCAATGACAAATTTGTTAAT 921
```

RESULT 11
US-10-782-020-4
; Sequence 4, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargis, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; METHODS FOR ITS USE

```
FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1806)
US-10-782-020-4

Query Match      5.5%; Score 117.6; DB 8; Length 1806;
Best Local Similarity 46.6%; Pred. No. 3.1e-16;
Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 532 TATCTTCATTATCTTGAGATTGGCTTACAGATAATCAATCCTAATAAACTTGCTGAC 591
DB 310 TATATACAAATTACGTAATGGAATGGAATAATGATTTGMAAACTCAAGGCTCAAGGTAG 369
QY 592 GTAGTTAAACAGTTCCACAGACGGGAAAGATTTCCTAACTTTAGCAGGGCTCTTA 651
DB 370 GTAGCTAATTACTATGAAAGCTCTTGACAGCGGCTGAAAGAGTATGCC---TCAATTT 426
QY 652 TCAGACAGAAAGCTGAATATTTATTTGCTTCAGTATGCAAGCTGCAAAATGTCAT 711
DB 427 GCAGTGAAGAAATTTGAAAGTACCTTTTAAGTCTCATGTGCAAGCTGCTAACTTCAT 486
QY 712 TTAATTACTATTAAGGACGAGTAATTAATTAATAAAGATGGGACTAGTGTCTACCG 771
DB 487 TTAATTATTAATTAAGAGATGTTGAGTTATGAAAGTGTGGGA----- 531
QY 772 TTGTATCCAGGTCAGGAGAACTGATTGTAACAGCGGTTAAAGCGAAATTAAGAG 831
DB 532 TGTGCGAGACAGAAATTAATAATTTATGATTAACAGATTA---GTATACCCATGAA 588
QY 832 TATACTAATTATGTTAGGAGTGGTATTAACAGGCTTTAGTCAATGATTAACAGCGGGT 891
DB 589 TACACAAATCATCTGTGTAATTTGATTAATTAAGAGCTTTAGAGATTTAAATAAGGT 648
QY 892 ACAAGTCTGAAGTTTGTGCGAAATTAATTAATTTGTAAGAGAAATGAGTGTGCGGTA 951
DB 649 TCTTCTATCAAGATTTGTAATTAATTAATTCGTTCCGTGAGAAATGACTCTTACGTT 708
QY 952 TTGATATTTATGCTAATTTCCACTTAATGATTTTAAATAATTCCTATTAGCAACAGT 1011
DB 709 TTGATATTCGTTGCTTTATTCCTGACACTATGATGTAACAACTTATCCAAATACACCGTT 768
QY 1012 GTAGAGTTAAGTGGGAAATTTATACAGATCCAGTGGGATTTTCAAGGGGAAAT---AT 1068
DB 769 GCTCAGCTAACAGGAAAGTTTATACGATCTTTTACTTAATTTTAAATCCTTAATTAATCAT 828
QY 1069 GGTGGGAAAGCTTTTATAGCTTTAATTCGTAAGAACCAATGGAACACCGGGAACCTGAT 1128
DB 829 TCTGTGCTCAATTAAGTTTATAGTACATGGAATAATGCAACAAATTAACATCCACAT 888
QY 1129 TTAGTTACTTGGCTTCAAGCTAATGATATATATGATTTCTATTCTTCAAGCTTGGT 1188
DB 889 CTATGGAATTTTAAAGATGCTAACAAATTTAATACAGATTGATATGCTGCGGAAGAAAC 948
QY 1189 TATCTTAGTGGCTGGGGGGAACCTGCTATTATGAAGCTTCAAGAGGTTAACCGGCT 1248
DB 949 TATATTATGGGGAAGACATGCGGTGAGCTCTTACATGTAGAGAGAGATATATAGATCA 1008
QY 1249 TTTCAACGTAATGCTGGAACCTACAGATTAATTCACGTAATATTTATTTTGGCAATACC 1308
DB 1009 CCTCTATATGTAGAGAGGCAAAATCAAGAGGTTCTTGAAGATTTTATTTTATGAGACC 1068
QY 1309 GATATATTTAAATTTATTTGATTAGTACATATGCAATGCAACCGTTTGTGGGTATTC 1368
```

```
DB 1069 GTTTTAAAGCTGTATTCMAAGCCGACTTAAGACCATTTACAGACGCTGACCAAGCTCT 1128
QY 1369 ATCCACGCGCATCTTGTGTTTACGTGAGAAATTTTTCGCAACACATTAATATCTTCTG 1428
DB 1129 CTTTAAATTTAGTACTTATGAGGAGTATGAAATTCACACTCTTACAGGTAATGTTATG 1188
QY 1429 TATGAGTAAACAGTTCTGGGTACTCACAGACAAATGAATCTGTGTTTACAGGATTAAT 1488
DB 1189 TATCGTGAAGAGATCGTATGATTTTAAATGAGTTGCGGCTTTAATCCAGTTGGG 1248
QY 1489 AAGATCTACCACTTACTGCTACAAATTAATCTCTATGATTAATCAATGGGATGTT 1548
DB 1249 TTAACCTATTAAGGATTAACATCAACGTTTATGTCATGCAACGTTTGTCTGAATTCGG 1308
QY 1549 CAAATGAAACCTCCAGAGTTAATGATTTGTTGACACATCAAGATTAATAAAGAT 1608
DB 1309 ACCCTTATTTAAACACAGGTGCACTTTTCTTGACACATGCTAGTCTGAAGAAACC 1368
QY 1609 AATGCAATTTATCCAGATTAATAATTAACGCAATTCCTGACGTAAGCTTTTGCCCTT 1668
DB 1369 AATACAAATGAATCAATATTTATTAACGCAATCCGTTAGTAAAGCATATCAAAATTTGG 1428
QY 1669 GCAGGTAC 1676
DB 1429 TCAGGCAC 1436

RESULT 12
US-10-782-020-2
; Sequence 2, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1890)
US-10-782-020-2

Query Match      5.5%; Score 117.6; DB 8; Length 1890;
Best Local Similarity 46.6%; Pred. No. 3.2e-16;
Matches 535; Conservative 0; Mismatches 589; Indels 24; Gaps 4;

QY 532 TATCTTCATTATCTTGAGATTGGCTTACAGATAATCAATCCTAATAAACTTGCTGAC 591
DB 394 TATATCAATTAAGTATGAAATGGAATAATGATATGAAATCAAAAGCTCAAGGTAG 453
QY 592 GTAGTTAAACAGTTCCACAGACGGGAAAGATTTCCTAACTTTAGAGGCTCATTA 651
DB 454 GTAGCTAATTACTATGAAGTCTTGACAGCGGCTGAAAGAGTATGCC---TCAATTT 510
QY 652 TCAGACAGAAAGCTGAATATTTATTTATTTGCTTACGATATGCAACCTGCAATGTGCAT 711
DB 511 GCAGTGAAGAAATTTGAAATGACCACTTTTAAGTCTATGATGCAACCTGCTAATCTTCAT 570
QY 712 TTAATTCTATTAAGGACGCAAGTTAATTAATAAAGATGGGACTAGTGTCTCAACCG 771
```


Db	571	TTATTTATTTATTAAGAGATGTTTCAGTTTATAGAAAGTGTGGGA-----	615
Qy	772	TTGTATCCAGGCTCAGGGAGACTGATTGTAAAGCGGTTAAAAGCAATATAAG	831
Db	616	TGTCGGAGCAGAAAATTAAATTTATATGATTAACAGATTAA---GTATACCATGAA	672
Qy	832	TATCTATAATTGTGTAGGGGTGTATTAACAAGGTTTAGTCAGATTAAGCAGCGGT	891
Db	673	TACCAAAATCATTGTGTAAATTGGTATATTAAGGACTTGAGATTAAAAATTAAGT	732
Qy	892	ACAAGTGTGAAGTTTGGTCGCAAAATTATATAATTTCTAGAGAAATGACGTTGGCGTA	951
Db	733	TCTTCTTATCAAGATGGGTACATTATATATGTTTCGTGATAGAAATGACCTTAACTGTT	792
Qy	952	TTGATATATATTGCTATATTTCCAACTATAGATTTGAAAAATATCCATTGCAACAGT	1011
Db	793	TTAATATACGTGCTTATATTCGCCGACATGATGACAACTTATCCAAATTAACACGTT	852
Qy	1012	GTAGAGTTAACTAGGGAATTTATATACAGATCCAGTGGGATATTTACAGGGGGAATTT--AT	1068
Db	853	GCTCAGCTAACAGAGGAAGTTTATACGATCCTTACTAATTTTAATCCTAATTAATCAT	912
Qy	1069	GGTTGGACGCTTTTATGCTTTATTCGTTACGTAAGCAAAATGGAACCGGGACCTGGT	1128
Db	913	TCTGTGTCCAATTACCTAGTTTATAGTACATGGAATAATGCAACAATTGAACTCCACAT	972
Qy	1129	TTAGTTACTTGAGCTCAAGCTATATATATATATATAGTCACTTCATTAATCTTCAAGTTGGT	1188
Db	973	CTGATGGAATTTTAAAGATGCTAACATTTTATACAGTTGTATATGTGTGGAAAGAAC	1032
Qy	1189	TATCTTAGTGGCTGGGGGGAACCTGTCATTATGAGAATTACAAAGGTTACGCTGTCT	1248
Db	1033	TATATATGGGAGGACATCGCGTACGCTTACCATGTAAGAGGAGGAATATTAAGATCA	1092
Qy	1249	TTTCAAGCTATGTCGGAACCTACAGATTAATATCCAGTAATATTTTGTGGCAATACC	1308
Db	1093	CCTCATATGTGTAGAGGCAAAATCMAAGGTTCCATAGATTTTATTTATGAGACC	1152
Qy	1309	GATATATTTAAATTAATTTCAATTAGCTGATATAGCATGACAAACGTTGTGGGTAATCA	1368
Db	1153	GTTTTTAAAGCGTTATCAAAAGCCGACTTAAGACATATACAGACCTCGACACAGTCTT	1212
Qy	1369	ATCCACGGCATCTTGTTTACGTCGAGAAATTTTCCGACACATTAATATCTTCTGTG	1428
Db	1213	CCTTTTAATTTAACGTAAGCTTAGAGGAGTAAGAAATCCACACTCCACAGTAGTATTATG	1272
Qy	1429	TATGAGTAAACAGTCTGGGGTACTCACAGCAAAATGAAATCTGTGTTACAGGATTAAT	1488
Db	1273	TATGTGAAAGAGATCCGTAGATTTCTTTTATAGTGGCCGCTTTTAATCCAGTGGG	1332
Qy	1489	AAGATCTACCACTAGTGTGTACAAATTACTCTCATAGATTATCAAAATGCGGCACTGTGT	1548
Db	1333	TTACTCTAATAGGTATACAGTACACGTTTATATGTCAATGCAACGTTTGTGTGTAATCTGGG	1392
Qy	1549	CAAAATGAACTCCAGAGTTAACGTATTTGGTTGGAACACATCAAGTATGAAAAAGAT	1608
Db	1393	ACCCTTAATTTAACACACAGTGCCATCTTTCTTGGACACATCGTAGCTGAAGAAACC	1452
Qy	1609	AATCAATTTATCCAGATTAATTAATTCGCAAAATTCCTGACATTAAGATCTTTGGCCTTACA	1668
Db	1453	AATACAATGGAATCAAAATTAATTAATTCGCAAAATCCCGTTAGTAAAGCATATCAAAATGGG	1512
Qy	1669	GCAGGTAC 1676	
Db	1513	TCAGGCAC 1520	

```

; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-020-1

```

Query Match	5.5%;	Score 117.6;	DB 8;	Length 2150;
Best Local Similarity	46.6%;	Pred. No. 3.4e-16;		
Matches 535; Conservative	0;	Mismatches 589;	Indels 24;	Gaps 4;

QY	532	TATCTTCATTA	CTTTGGAGAT	TTGGCTTA	CAAGATTA	ATCAAT	TCCTAA	AAAACTT	GGCTGAC	591	
Db	694	TATATACATTA	CGTATGAT	TGGGAAAA	TGATTT	TGAAA	CTCAAG	GCTCAAG	GTTAG	753	
QY	592	GTAGTTAA	CAGTTC	CAAGCA	CGGAGAA	GATTT	CACTAA	CTTTAG	CAGGGTCA	651	
Db	754	GTACTATTA	TCTATG	AAAGCTT	GGACGCG	GTGAA	AGGAT	ATGCC---	TCAATTT	810	
QY	652	TCAAGAC	AGAAAGCT	GAAATAT	TATAT	TTCCTA	CGTATG	CAAGCTG	CAATGTGCAT	711	
Db	811	GCAGTGA	GAGATTT	TGAAGT	ACCACTTT	TA	CTGTATG	CAAGCTG	CTAATCTTCAT	870	
QY	712	TTATTTACT	TATTAAG	GCACG	AGTTAA	TAT	AAAAA	AGAT	TGGGCACT	ATGTGCCACG	771
Db	871	TTATTTATTA	TATMA	GAGATG	TTTCAGTT	TAT	TGAAA	AGTGT	TTGGGGA-----	915	
QY	772	TTGTATC	ACAGGCT	CAGGGAG	ACGAT	TTGT	TAC	CAGGCGTT	AAAGCGAAAT	831	
Db	916	TGGTGG	CAGCAAAATTT	AAATTT	TAT	TATGAT	TAA	CAGATTA---G	TATACCA	972	
QY	832	TATACTA	TATTTG	TGTAG	GCGTGT	TAT	TAA	CAGGGTT	TGAT	TGAT	891
Db	973	TACCAAT	ATCATCT	TGT	TATTA	TTGGT	TAT	TAA	GAGCTTG	GAGATTT	1032
QY	892	ACAAGT	CGTGAAGTT	TGGT	CGAAA	TTT	TAT	TAA	TTTGGT	TAGAAAT	951
Db	1033	TCTTCTTA	TATCA	AGATTGG	TACAA	TTAT	TAT	TCGTT	CGT	TAGAAAG	1092
QY	952	TTGATAT	TATTTG	CTATAT	TTCCAA	CTT	TGAT	TTTGAAA	AAAT	TCAT	1011
Db	1093	TTAGATAT	CGTTC	TTATTT	CCGCA	CTAT	GAT	GTAT	CAAACTTA	TCCAA	1152
QY	1012	GTAGAGT	TAACT	TAAGGAA	ATTTAT	TAC	AGAT	CAGT	GGGATTT	CA	1068
Db	1153	GCTCAG	CTAA	CAAGGAA	GTTTAT	TAC	GAT	TCCTT	ACT	TAT	1212
QY	1069	GGTGGGA	CGGTTTT	TTTAA	GCTTTA	TAT	TTCG	TAG	ACCAAT	TGAA	1128
Db	1213	TCTGTGT	CTCA	ATTAC	CTA	AGTTT	TAT	TAG	CAAT	TGAAA	1272
QY	1129	TTAGT	ACTT	TGGCTT	CAAGCT	TAT	TAG	TAT	TAT	TAT	1188
Db	1273	CTGAT	GAAATTTT	TAA	GAT	CTT	CA	ATT	TAT	TAC	1332
QY	1189	TATCT	TAGT	CGCTGG	GGGGA	AC	TG	CAT	TAT	TAA	1248
Db	1333	TATTT	TTTGGG	AGGAC	AT	CGGCT	GT	AC	CTT	TAC	1392
QY	1249	TTTCA	ACG	TAT	GTCTG	CA	AT	CTT	CA	GAT	1308

Db 1393 CCTTATATGATAGAGAGGCAATCAAGGCTCTAGAGATTTTATTTTATGACCC 1452
QY 1309 GATATATTTTAAATTTATTTATTTAGTATGCAATGCAACCGTTTGTGGTATTTCA 1368
Db 1453 GTTTTAAAGACGTTATCAAGCCGACTTAAGACATTAAGAGCCCTGACCAAGCTCT 1512
QY 1369 ATCCAGGCACTTTGTTTACGCGCAAGATTTTTCGACACACTTAATCTTCTG 1428
Db 1513 CTTTATTTATTTACCTAGCTTATGAGGAGTGAATTTCACTCTTACAGGATGTTATG 1572
QY 1429 TATAGGTTAAACAGTCTGGGTACTCAAGCAATGATGATGCTTACAGATTAAT 1488
Db 1573 TATGTTAAAGAGATCGTATGATTTCTTTATGATGTCGCGCTTTAATCCAGTGG 1632
QY 1489 AAGATCTACCACTAGTCTGTAATTAATTAATCTGATGATTAATGAGGAGTGT 1548
Db 1633 TTACCTATAGGATACAGTACCGTTTATGTCATGCAACGTTTGTGTAATCTGG 1692
QY 1549 CAAATGAAACCTTCAGAGTTAACGTAATTTGTTGCAACATACAGTATGAAAAAGAT 1608
Db 1693 ACCCTTATTTTAAACACAGGCGCATCTTTCTTGACACATCGTAGTGAAGAAAC 1752
QY 1609 AATGATTTATTCAGATTAATAATAGCAATTCCTGAGTAAAGCTTTTGCCTACCA 1668
Db 1753 AATACATTTGATCAATTAATTTATTAACGAAATCCGTTAGTAAAGATATCAATTTGG 1812
QY 1669 GCAGGTAC 1676
Db 1813 TCAGGCAC 1820

RESULT 14
US-10-428-961-62
; Sequence 62, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rel
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rudar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-62

Query Match 5.4%; Score 116.8; DB 6; Length 3684;
Best Local Similarity 55.0%; Pred. No. 6,7e-16;
Matches 310; Conservative 0; Mismatches 227; Indels 27; Gaps 3;
QY 532 TATCTTATATTTATTTGAGATTTGCTTACAGATTAATCAATCTTAAATCTTAAATCTTGCATC 591
Db 400 TATCAACAGTCACTGTAAGATTTGGCTAGAAACCGTATGATGCAAGAAAGAGTGT 459
QY 592 GTAGTTAAAGATTTCCAGACGGGAAAGAAATTTCACTAACTTTTGAAGAGGCTATTA 651
Db 460 CTTTATACCAAAATATATAGCTTAGAATTTTCTTATGATGAGATGCGCTTTTCGCA 519
QY 652 TCAAGACAGAAAGCTGAATATTTATTTGCTTACGATGCAAGCTGCAATGTCAT 711

Db 520 ATTGAACCAAGAAAGTTCCATTTATATG---GTATATGCTCAAGCTGCAATTTACAC 576
QY 712 TTAATCTATTTAAAGGACGAGTTAAATATTAATAAAGATGGGACTAGTGTCCACCG 771
Db 577 CTATTTATTTAGAGATGCTCTCTTTTGTAGTGAATTTGGGCTTACATCCCAAGAA 636
QY 772 TTGATTCAGAGGTTCAGGAGAACTGATTTGTAAGAGCGGTTTAAAGCAAAATTAAGAG 831
Db 637 ATTCAACG-----TTATTTATGAGCGCAAGTGTGAAAAACGACAGAA 678
QY 832 TATCTAATTTATTTGTAGGCGGTGTATTAACAAGGTTTATGATGATTAAGACAGCGCGGT 891
Db 679 TATCTGATTTATTTGCGACAGATGTATTAACGGGTTTAAATTAATTTGACA-----GGG 732
QY 892 ACAAGTCTGAAGTTTGTTCGAATTTAATTAATTTTGTAGAGAAATGACGTTGGCGCTA 951
Db 733 ACAATGCTGAAGTTTGTTCGATTAATTAATTAATTTTGTAGAGAAATGACGTTAGAGAT 792
QY 952 TTGATTTATTTTGTCTATTTTCCACTTATGATTTTGAATAATATTCATTTAGCAACAGT 1011
Db 793 TTGATCTAGTGTGACATATCCCAAGCTATGACACGCGTGTATTCATCAATGATACAGT 852
QY 1012 GTAGGTTAATCTAGGAAATTTATACAGATCCAGTGGATATTCAGGGGAAATTAATGT 1071
Db 853 GCTCAATTTAACAAGAAATTTATACAGATTCATTTGAGAGAAACAATGACCTTCAGGA 912
QY 1072 TGGAAACGCTTTTGTAGCTTTAAT 1095
Db 913 TTTGCAAGTACGAATTTGTTAAT 936

RESULT 15
US-10-665-460A-7
; Sequence 7, Application US/10665460A
; Publication No. US2004009693A1
; GENERAL INFORMATION:
; APPLICANT: Freysinet, Georges
; APPLICANT: Rang, Cecile
; APPLICANT: Futos, Roger
; TITLE OF INVENTION: Pepsin-sensitive modified Bacillus thuringiensis insecticidal
; FILE REFERENCE: A35992-PCT-USA-A (072667.0191)
; CURRENT APPLICATION NUMBER: US/10/665,460A
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/FR02/00772
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR 01/03691
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence description: Cry9Ca1 Glu-164
; NAME/KEY: CDS
; LOCATION: (1)..(2019)
US-10-665-460A-7

Query Match 5.3%; Score 113.4; DB 7; Length 2019;
Best Local Similarity 55.8%; Pred. No. 3e-15;
Matches 294; Conservative 0; Mismatches 206; Indels 27; Gaps 3;
QY 527 ATATATATCTTATTTATTTGAGATTTGGCTTACAGATTAATCAATCTTAAATCTTAAATCTTGCATC 586
Db 440 ATGTATATCAACGTTCCCTTCAAAATTTGTTGTGCTATGCAATGATGTAAGAAATTTTA 499
QY 587 CTGACGTAGTTAAACGTTCCAGACGGGAAAGAAATTTCACTAACTTTTGAAGAGGT 646
Db 500 GTTGTGTGCTGCTCAATTTATAGCTTTAGACCTTGAATTTTGTATATGCTATTCCA---T 556

```

QY      647  CATTATCAGACAGAAAAGCTGAATATTTATTATGCTACGTATGTCAGCTGCAATG 706
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      557  TGTTCACGTAATGGAACAGCAGGTTCATTACTGTGATATAGCAACAAGCTGTGAATT 616
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      707  TGCATTATTAATCTATTAAAGGACGCAAGTTAAATATAAAAAAGATGGGACTAGTGTGTC 766
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      617  TACATTTGTATATTAATAAGATGCATCTCTTTTGGAGAAAGATGGGGATTCA----- 670
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      767  CACCGTTGATCCAGGGTCAGGGAGAACTGATTGTAAAGACGCGTTAAAAAGCAAAATTA 826
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      671  -----CACAGGGGGAATTTCCACATATTATGACCGTCAATTGGAATTAACCG 718
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      827  AAGATATATCTAATTTATGTAAGGAGTATTAACAAGGTTAGATCAGATAAGACAG 886
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      719  CTAACTACCTAATTTACTGTGAACCTTGTATTAATACAGGTTAGATCGTTAAGA---- 774
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      887  CCGGTAACAAGTCTGAAGTTTGTGCGAATTTAATAAATTTCTAGAGAAATGACGTGG 946
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      775  --GGAACAATATCTGAAGTTGTTAAGATATCATCAATTCGTAGAGAAATGACTTTAG 832
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      947  CGGTATTGATATTTATGCTAATTTCCAACTTATGATTTGAAAAATATCCATTAGCAA 1006
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      833  TGGTATTAGATGTGGCGCTATTTCCATATATGATGTACGACTTTATCCAAACGGGAT 892
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1007 CAAGTGAAGTTAACTAGGGAATTATACAGATCCAGTGGGATAT 1053
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      893  CAATCCACAGCTTACAGTGAAGTATATACAGATCCGATTGTATTT 939
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: December 19, 2005, 13:41:15
 Job time : 1174.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:27:04 ; Search time 267.352 Seconds

(Without alignments)
14261.593 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataataatgctt.....atagttattatcaattaa 2145

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/1 COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5 COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/H COMB.seq: *
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq: *
7: /cgn2_6/ptodata/1/ina/PP COMB.seq: *
8: /cgn2_6/ptodata/1/ina/RE COMB.seq: *
9: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172.4	8.0	3468	3 US-09-001-982-9	Sequence 9, Appl1
2	172.4	8.0	3468	3 US-09-668-650-9	Sequence 9, Appl1
3	172.4	8.0	3471	3 US-09-002-285-71	Sequence 71, Appl1
4	172.4	8.0	3471	3 US-09-589-477-71	Sequence 71, Appl1
5	172.4	8.0	3471	3 US-10-099-385A-71	Sequence 71, Appl1
6	172.4	8.0	3726	3 US-09-001-982-11	Sequence 11, Appl1
7	172.4	8.0	3726	3 US-09-668-650-11	Sequence 11, Appl1
8	162.8	7.6	2407	3 US-09-661-322A-29	Sequence 29, Appl1
9	119.8	5.5	1959	3 US-09-661-322A-5	Sequence 5, Appl1
10	118.2	5.5	3934	2 US-08-100-709-3	Sequence 3, Appl1
11	118.2	5.5	3934	2 US-08-176-865-3	Sequence 3, Appl1
12	118.2	5.5	3934	2 US-08-474-038-3	Sequence 3, Appl1
13	118.2	5.5	3934	2 US-08-779-046-3	Sequence 3, Appl1
14	118.2	5.5	3934	2 US-08-881-340-3	Sequence 3, Appl1
15	116.8	5.4	3684	2 US-08-448-170-7	Sequence 7, Appl1
16	116.8	5.4	3684	2 US-08-961-803-5	Sequence 5, Appl1
17	116.8	5.4	3684	3 US-09-661-322A-62	Sequence 62, Appl1
18	112.4	5.2	4173	3 US-09-661-322A-37	Sequence 37, Appl1
19	111.8	5.2	1897	3 US-09-363-970-5	Sequence 5, Appl1
20	111.8	5.2	3471	3 US-09-002-285-73	Sequence 73, Appl1
21	111.8	5.2	3471	3 US-09-589-477-73	Sequence 73, Appl1
22	111.8	5.2	3471	3 US-09-661-322A-27	Sequence 27, Appl1
23	111.8	5.2	3471	3 US-10-099-385A-73	Sequence 73, Appl1
24	111.8	5.2	4344	2 US-08-532-547-4	Sequence 4, Appl1

25	111.8	5.2	4344	2 US-08-379-656B-4	Sequence 4, Appl1
26	111.8	5.2	4344	3 US-08-455-838-4	Sequence 4, Appl1
27	111.8	5.2	4344	3 US-09-019-809-4	Sequence 4, Appl1
28	111.8	5.2	4344	3 US-09-471-177-4	Sequence 4, Appl1
29	111.8	5.2	4344	3 US-09-220-806-4	Sequence 4, Appl1
30	110.8	5.2	1561	2 US-08-532-547-2	Sequence 2, Appl1
31	110.8	5.2	1561	2 US-08-379-656B-2	Sequence 2, Appl1
32	110.8	5.2	1561	3 US-08-455-838-2	Sequence 2, Appl1
33	110.8	5.2	1561	3 US-09-019-809-2	Sequence 2, Appl1
34	110.8	5.2	1561	3 US-09-471-177-2	Sequence 2, Appl1
35	110.8	5.2	1561	3 US-09-220-806-2	Sequence 2, Appl1
36	107.8	5.0	1607	3 US-08-286-870A-5	Sequence 5, Appl1
37	107.8	5.0	1946	3 US-08-286-870A-3	Sequence 3, Appl1
38	107.8	5.0	2965	2 US-08-460-570-1	Sequence 1, Appl1
39	107.8	5.0	2965	2 US-08-460-570-2	Sequence 1, Appl1
40	107.8	5.0	2965	2 US-08-286-870A-1	Sequence 1, Appl1
41	107.8	5.0	2965	3 US-08-286-870A-2	Sequence 2, Appl1
42	105.2	4.9	3507	2 US-08-315-468-3	Sequence 3, Appl1
43	104.4	4.9	4074	2 US-08-377-690-1	Sequence 1, Appl1
44	103.4	4.8	3414	2 US-07-373-320-3	Sequence 3, Appl1
45	101.8	4.7	1953	2 US-08-315-468-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-001-982-9
Sequence 9, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8589
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468

US-09-001-982-9

Query Match 8.0%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 5,6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGGAAATCAGTCTCGAATATATAGTAACTATTTGGACATACCTTATACATTTCTGCTGAAC 346
158 GCGATGACGAAAGAAAGACGATATCTATTTGGACAAACCATATGCTCTTATACAGCAC 217
347 CCGGATATAGTGAATTCCTGTAATATTTT-----CAATATATAACAAACTCATTCGCT 400
218 CTCTCTTACTGATTAATTTCAATAGTATAGACCTTATAGGTAAGTAAAGTACTAGAGGTA 277
401 CTCTGCTCAATCTGTCGACGCACTTCTATATGATGATTTAGTATCTATATTCGTAAG 460
278 GATGATGACAAATCCAAATGCAATTTGCTATATGATGATCTTATATCTATATTAATTTAC 337
461 AGGTAGACGAGACGCTTAAAGTACGAGGCTGACATTTTGGAGGTAAGTATGACTGCTT 520
338 GGGTAACTGAGATGCTTTTAAATGATGAGGATTCGATTTTAAATGCTTCTATCTTAT 397
521 ATCAAGATTATATCTTC-----ATTATCTTGAAGATTGCTTACAGATA 565
398 ACAGAACTATTTAGAGGCTCTGGATAGTGAATAAGATCTTAATTCGCTTCTGCTG 457
566 AATCAAACTCTAAATAAATCTGCTGACGCTTAAACGTTCCAGACGCGGAAGAAAT 625
458 AAGAACTCGGTACTCGTTTAAATGCGCCACTCAGAAATTTGATGAATTTTAAACCCGAG 517
626 TCACATACTTTAGCAGGCTCATTTATCAGACAGAAAGCTGAATATTTATTTATGCTTA 685
518 GGTCTTTAAGAAATGGGCTGCTGTTAGTACGACAAATGCGCAAAATTTATTTATTCCTT 577
686 GGTATGTCAGGCTGCAATATGTCATTTATTTATTTAGGAGCGCAGTTAAATATATATAA 745
578 CTCTTGCAGCGCTGCAATTTTTCATTTATTTACTATTAAGGAGTCTACTAGATATGGCA 637
746 AAGAAATGGGACATATGATGTCACCGTTTATCCAGGCTGAGGAACTGATTTGTAAG 805
638 CTAAATGGGGGCTATATCAAAATGCTAACCTTTTATA-----ATTATCAAT 682
806 AGCGTTTAAAGCGAAATATTAAGATATTAATTAATTTAGGCTGATTAACAG 865
683 CAAACTAGTAAAGCTTATTAAGATATTAATTTATTTGCTATTTGCTATTAATGAG 742
866 GTTTAATCATGATTAAGACAGGCGGTAACAATGCTGAAGTTTGTGCAATTTTAAATTAAT 925
743 GTTTCAACGAATTAAGACAGGCACTAGTGTCTACAGCTTGTGTTAGAAATTTCAATGAT 802
926 TTGCTAGAAATGAGCTTGGCGTATTTGATATTTATTTGCTATATTTCCAACTTAATGAT 985
803 ATGTGAGAGATGACATTTATGATTTATTAATTAATGATCATTTTCAAGCTTGATA 862
986 TTGAAATATTCATTAAGACAGATGATTAAGTAACTAGAGAAATTTATATAGATCCAG 1045
863 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 922
1046 TGGGATATTCAGGGGGAATTAATGTTGGAA 1077
923 TTGTTTGTGATCGATGATGATCTTATGAGGA 954

RESULT 2

US-09-668-650-9

Sequence 9, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Boesch, Hendrick J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/668,650

FILING DATE: 22-Sep-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/001,982

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/602,737

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 3468 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3468

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-668-650-9

Query Match 8.0%; Score 172.4; DB 3; Length 3468;
Best Local Similarity 54.2%; Pred. No. 5,6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

287 GGGAAATCAGTCTCGAATATATAGTAACTATTTGGACATACCTTATACATTTCTGCTGAAC 346
158 GCGATGACGAAAGAAAGACGATATCTATTTGGACAAACCATATGCTCTTATACAGCAC 217
347 CCGGATATAGTGAATTCCTGTAATATTTT-----CAATATATAACAAACTCATTCGCT 400
218 CTCTCTTACTGATTAATTTCAATAGTATAGACCTTATAGGTAAGTAAAGTACTAGAGGTA 277
401 CTCTGCTCAATCTGTCGACGACCTTCTATATGATTTAGTATCTATATTTGTAAG 460
278 GATGATGACAAATCCAAATGCAATTTGCTATATGATGATCTTATATCTATATTAATTTAC 337
461 AGGTAGACGAGACGCTTAAAGTACGAGGCTGACATTTTGGAGGTAAGTATGACTGCTT 520
338 GGGTAACTGAGATGCTTTTAAATGATGAGGATTTGAGATTTTAAATGCTTCTATCTTAT 397
521 ATCAAGATTATATCTTC-----ATTATCTTGAAGATTGCTTACAGATA 565
398 ACAGAACTATTTAGAGGCTCTGATAGCTGGAATTAAGATCTTAATTCGCTTCTGCTG 457
566 AATCAAACTCTAAATAAATCTGCTGACGATTAACAGTTCAAGTCAAGACGCGGAAGAAAT 625
458 AAGAACTCGTACTGCTTTTAAATGATGAGGATTCGCAATTTGATGATATTTTAAACCGAG 517
626 TCACATACTTTAGCAGGCTCATTTATCAGACAGAAAGCTGAATATTTATTTATGCTTA 685
518 GGTCTTTAAGAAATGGGCTGCTTATGCTAGACAAATGCGCAAAATTTATTTATTAATCTT 577

```

QY 686 CGTATGCGCAAGCTGCAAAATGCTATTATTACTTATAGGAGCGAGTTAAATATATAA 745
Db 578 CTTTGGGAGGCTGCAATTTTTCATTAATTAAGGAGCTACTAGATATGGCA 637
QY 746 AAGAATGGGAGCTAGTGTGTCACCGTGTATCCAGGGGTGAGGAGAACTAATTGTACG 805
Db 638 CTAATTGGGGCTTATCAATCTCTACCTTTTATA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGCGAAATTAAGATTAATTAATTTATGAGGTGTATTAACAAG 865
Db 683 CAAATAGTAGTACTTATTAATTAATTAATTAATTTATGAGGTGTATTAACAAG 742
QY 866 GTTATGATCAGATTAAGACGCGGGTACAGTCTGAACTTTGTCGAAATTAATAAT 925
Db 743 GTTTCACGAACTAAGACAAAGAGGCACTAGTGTACAGCTTGTAGAAATTTCAATGAT 802
QY 926 TTGATGAAATAGCTGCGGGTATTTGATATTATTTGCTAATTTTCCACTATGATT 985
Db 803 ATCTAGAGATGATACATTTGATTTAGATTAAGATCAATTTTCAAGTCTTATATA 862
QY 986 TTGAAAAATTCCTTAGCAACAAGTATGAGTTAAGGGAATTTATACAGATCCAG 1045
Db 863 TTAATAATTAACCAATGAAGACAGATTTTCAGTTGAGTGGTCAATTTATCAATCCA 922
QY 1046 TGGATATTCAGGGGGAATTAATGCTTGGGAA 1077
Db 923 TTGGTTTGTACATCTAGTAGTCTTAGGGA 954

```

RESULT 3

US-09-002-285-71
Sequence 71, Application US/09002285
Patent No. 6369213

GENERAL INFORMATION:

APPLICANT: Schneck, H. Ernest
APPLICANT: Micker, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Peets
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-002-285-71

Query Match 8.0%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 5.6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

```

QY 287 GGGATATGCTCGGATATATGTAATTAATGGGACATACCTTAACAATCTTGTAGAAC 346
Db 158 GCGATGACGAGAAAGAGAGATCTATTTGGGACAAACCAATGCTCTTATACACACAC 217
QY 347 CCGGTATAGGTGGAATCCGTATATTTT-----CAATTAATAACAATCTACCTCCGT 400
Db 218 CTCTCTTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 277
QY 401 CTCTGCTCAATCTGTGCGACACTTCTATATGATTTAGTATCTATATTTGTTAAAG 460
Db 278 GTATGACAAATCATATCAGATTTGCTATATGTAATTTATCTATATTTATTTAC 337
QY 461 AGTAGACGAGCGTGTAAAGTACGCGGGTTCAGATTTTGAAGGTAATGACTGCTT 520
Db 338 GGGTATGTCAGAGGTGTTTAAATGATGGGATTTGATTTTATGTTGTTGTTGTTAT 397
QY 521 ATCAAGTATTAATCTT-----ATTATCTTGAAGATTTGCTTACAGATA 565
Db 398 ACAGAACTATTTAGAGGCTCTGTGATGCTGAATTAAGAAATCTTAATCTGCTCTG 457
QY 566 AATCAAAATCTTAAATACTGTCAGCTGATTTAAACAGTTTCAAGCAGGAGAAAGATT 625
Db 458 AAGAATCCGATCTGCTTTTGAATGCGCCAGCTCAAGATTTGAATTTTAAACCGAG 517
QY 626 TCACTAACTTTAGACGCGTCAATTAACAAGAGAGTGAATATTAATTTATGCTTA 685
Db 518 GGTCTTTAAGAAATGCGCTGCTGTTAGCTAGACAAATGCGCAATATTAATTTACCTT 577
QY 686 CGTATGCGCAAGCTGCAAAATGCTATTTATTAATTAAGGACGCTTAATTAATAA 745
Db 578 CTTTGGAGCGCTGCAATTTTCCATTTATTAATTAATTAATTAATTAATTAATTAAT 637
QY 746 AAGAATGGGAGCTAGTGTGTCACCGTGTATCCAGGGGTGAGGAGAACTGATTTGACG 805
Db 638 CTAATTGGGGCTATTAACAATGCTACACTTTTATA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGCGAAATTAAGATTAATTAATTTATGAGGTGTATTAACAAG 865
Db 683 CAAATAGTAGTACTTATTAAGAACTATTAATTAATTTATGAGGTGTATTAACAAG 742
QY 866 GTTATGATCAGATTAAGACGCGGGTACAGTCTGAACTTTGTCGAAATTAATAAT 925
Db 743 GTTTCACGAACTAAGACAAAGGCACTAGTGTCTACAGCTTGTAGAAATTTCAATGAT 802
QY 926 TTGATGAAATAGACGTTGGCGGTAATTTGATTTATTTGCTAATTTTCCACTATGATT 985
Db 803 ATCTAGAGATGATACATTTGATTTATTAATTAATTAATTTATGAGGTGTATTAACAAG 742
QY 986 TTGAAAAATTCCTTAGCAACAAGTATGAGTTAAGGGAATTTATACAGATCCAG 1045
Db 863 TTAATAATTAACCAATGAAGACAGATTTTCAGTTGAGTGGTCAATTTATCAATCCA 922
QY 1046 TGGATATTCAGGGGGAATTAATGCTTGGGAA 1077
Db 923 TTGGTTTGTACATCTAGTAGTCTTAGGGA 954

```

RESULT 4

US-09-589-477-71
Sequence 71, Application US/09589477
Patent No. 6570005

GENERAL INFORMATION:
APPLICANT: Schneck, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-589-477-71

Query Match 8.0%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 5.6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

Db 287 GGGATATAGTCTGGATATAGTACTTTGGGACATACCTTATACAACTTCTGCTAGAAC 346
158 GCGATGACGAGAAAGAGCATCTATGCGACACCATAGCTCTCTATACAGACAC 217
347 CCGATATAGTGGATCTGATATATTTT-----CAATAATAACAACCTATTCGCT 400
218 CTCTCTTACTGATTAATTCATATATATGACCTTATAGGTAAGTCTAGAGAGTA 277
401 CTCTGCTCATCTGTCGACGACACTTCTATATGATTTAGTATCTATTAATTCGTAAG 460
278 GTAGTGCACATCATATCAGATTGCTATATGATGACTATATCTATATGATTTAC 337
461 AGGTAGCGAGCGGTGTAAAGTACGGGGTTCAGATTTTGGAGGGTGAATGACTGCTT 520
338 GGGTAAGTCAAGAGGTTTAAATGATGGAATGCGAGATTTTAAATGAGTTCGACTCTAT 397
521 ATCAAGATTATTAATCTC-----ATTATCTGAGAGTTGGCTTACAGATA 565
398 ACAGAACTATTAGAGGCTCTGATAGCTGGAATTAAGATCTTAATTTGCTTCTCTG 457
566 AATCAATCTTAATAAACTTGCTGACGTAGTTAAACAGATTCACAGACGGGAGAGATTT 625

Db 458 AAGAACTCCGTAAGTCTGTTTAGAATGCGGACATCAAAATTTGATTAATTTTAAACCCGAG 517
626 TCACTAACTTTTACAGAGGCTCATTTATCAAGACAGAAAGCTGAATATTTATTTGCTTA 665
518 GGTCTTTAAGAAATGCTGCTGTTTGTAGCAAAATCCCAATATTAATTAATTCCTT 577
686 CGTATGTCAGAGTGCAGAAATGTCATTTATCTATTAAGGAGCGAGTTAAATATATAA 745
578 CTCTTCGAGCGCTGCATTTTCCATTTATTTACTTAAGGATGCTACTAGATAGGCA 637
746 AAGATGCGGACTAGTGTGTCACCGTGTATCCAGGGTCAAGGAACTGATTTGTAAG 805
638 CTAAATGGGGGCTATCAATAGCTACACTTTATAA-----ATTATCAAT 682
806 AGCGTTTAAAGCGGAAATTAAGAGTATCTAATTTATTTGTAGGCTGATTAACAAG 865
683 CAAACTAGTAGGCTTATTTGAATATTAATCAATTAATTTGCGTACATTTGATTAATCGAG 742
866 GTTTAGATCAGATTAAGACAGCGGGGTACAGTGTGAAGTTTGGTGAATTTAATAAT 925
743 GTTCAACGAACTAAGACACAGGCACTAGTCTACAGCTTGTTAGATTTCAATGAT 802
926 TTGATAGAAATAGAGCTTGGCGTATTTGATTAATTTCTATATTTTCAACTTATGAT 965
803 ATCGTAGAGAGATGATGATGATGATTAATTTAGATTAATGATTTCAAGCTTGATTA 862
986 TTGAATAATTTCCATTTAGCAACAGTGTAGATTAATCTAGGAAATTTTATAGATCCAG 1045
863 TTAATAATTTACCAATTAAGAAACGATTTTCAAGTGTAGGCTGATTTTATACAGATCCA 922
1046 TGGATATTTACAGGGGAAATTAATGTTGGAAA 1077
923 TTGTTTGTACATCTGATGATTTAGGGGA 954

RESULT 5
US-10-099-285A-71
Sequence 71, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schneck, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285A-71

Query Match .8.0%; Score 172.4; DB 3; Length 3471;
Best Local Similarity 54.2%; Pred. No. 5.6e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATACGCTCGGATATAGTAACTATGGGACATACCTTAACTTCTGCTAGAAC 346
DB 158 GCGATGAGCAAAAGACAGTATCTATTGGGACACATAGCTCTCTTATCAGACAC 217
QY 347 CCGGTATAGTGAATTCCTGTAATTTT-----CAATATAAACAACCTCAATCCGT 400
DB 218 CTCTCTTACTGATTAATTAATGAGCTTATAGCTTATAGTAACTAGAGGTA 277
QY 401 CTCTGTCATCTGTGGACAGCACTTCTATATGATTTAGTATCTATATGCTAAAG 460
DB 278 GTATGACATATCATATCAGATTGCTATATATGATTTATCTATATATGATTTAC 337
QY 461 AGGTAGAAGAGCGGTATAGTACGCGGTGGAGATTTGAGGTTGAATGACCTCT 520
DB 338 GGGTAACTGAGAGTCTTAAATGATGGAATGCAATTTTAATGTTGTAATCTTAT 397
QY 521 ATCAAGTTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565
DB 398 ACAGAACTATTAAGAGCTCTGATAGCTGGAATAGAAATCTTAATCTGCTCTG 457
QY 566 ATCAAAATCCTAATAAACTGCTGACGATTAACAGTTCCAGACGGAAGAAAT 625
DB 458 AAGAACTCCGTAATCGTTTGAATGCGGACCTGAAATTTGATGAAATTTTAA 517
QY 626 TCACTAACTTTTGAAGGCTATATCAAGACAAAGCTGAATTTATTTGCTTA 685
DB 518 GGTCTTAAGAAATGGGCTCGTTAGCTAGACAAATGCGCAATTTATTTACTT 577
QY 686 CGTATGCAAGCTGCAATGTCATTTATTTACTTATTAAGGACGCTTAATATAA 745
DB 578 CTTTGGAGCGCTGCAATTTTCCATTATTACTTAAGGAGCTTACAGATATGCA 637
QY 746 AAGAACTGAGCTAGTGTGTCACCGTTGATCCAGGCTCAGGGAAGATTTGTA 805
DB 638 CTAAATGGGGCTTATCAATGCTACACCTTTTAA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGCGAAATTAAGAGATTAATTTATTTGATGAGGTGATTAACAG 865
DB 683 CAATACTAGTAGCTTATGAATCTATATCTGATTTTGGGATCAATTTGATATGAG 742
QY 866 GTTTAGTCAATAGACAGCGGCTCAAGTGTGAAGTTTGGTCAAAATTTAATAAT 925
DB 743 GTTTCACGAACTAAGACAGAGGCACTAGCTCAAGCTTGTTGAATTTCAATGAT 802
QY 926 TTGCTAGAAATGACGTTGGCGTATTTGATATTTATTTGCAATTTCAATTAAT 985
DB 803 ATGCTAAGAGATCACTTATGATTTATTAATTAAGTACATCTTTTCAAGCTTATA 862
QY 986 TTGAAATATTCATTAAGCAAGGTGATTAATCTAGGAAATTTATACAGATCCAG 1045
DB 863 TTACTAATTAAGCAATTAAGATTTTCAAGTGAAGGCTATTTATACAGATCCAA 922
QY 1046 TGGATATTCAGGCGGAAATTTATGCTTGGAA 1077

DB 923 TTGCTTTGATCATCTAGTATGCTTAAAGGGA 954

RESULT 6
US-09-001-982-11
Sequence 11, Application US/09001982
Patent No. 6204246
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
APPLICANT: Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6204246artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3726
US-09-001-982-11

Query Match .8.0%; Score 172.4; DB 3; Length 3726;
Best Local Similarity 54.2%; Pred. No. 5.7e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATACGCTCGGATATAGTAACTATGGGACATACCTTAACTTCTGCTAGAAC 346
DB 158 GCGATGAGCAAAAGACAGTATCTATTGGGACACATAGCTCTCTTATCAGACAC 217
QY 347 CCGGTATAGTGAATTCCTGTAATTTT-----CAATATAAACAACCTCAATCCGT 400
DB 218 CTCTCTTACTGATTAATTAATGAGCTTATAGCTTATAGCTTATAGTAACTAGAGGTA 277
QY 401 CTCTGTCATCTGTGGACAGCACTTCTATATGATTTAGTATCTATATGCTAAAG 460
DB 278 GTATGACATATCATATCAGATTGCTATATATGATTTATCTATATATGATTTAC 337
QY 461 AGGTAGAAGAGCGGTATAGTACGCGGTGGAGATTTGAGGTTGAATGACCTCT 520
DB 338 GGGTAACTGAGAGTCTTAAATGATGGAATGCAATTTTAATGTTGTAATCTTAT 397
QY 521 ATCAAGTTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565

Db 398 ACAGAACTATTGAGGCTCTGAGATAGCTGAATAGAAATCTTAATTCCTTCCTG 457
QY 566 AATCAATCTTAAAACTTGTAGAGTAGTAAACAGTCCAGACGGAGAGAAATT 625
Db 458 AAGAACTCCGTACTCGTTTAGAATCGCCAGCTCAGAAITTTAGAAATTTTACC 517
QY 626 TCACATACTTTTGAAGGCTCATTTATCAAGACAGAAAGCTGAAATTTATTTCC 685
Db 518 GGTCTTTAAGAAATGGGCTCGTTAGCTAGCAAAAATGCCAAATTTATTTACCT 577
QY 686 CGATGTGCAAGCTGCAGATGTGATTTATTTACTTTAAGGACGCAATTAATTA 745
Db 578 CTTTTCGAGCGCTGATTTTTCATTTATTTACTTAAGAGAGTACTAGATATGCG 637
QY 746 AAGATGGGACTAGTGTGTCCACCGTGTACAGGGTCAAGGAGAACTGATTTAG 805
Db 638 CTAAATGGGGCTATACATGCTACACCTTTTAA-----ATTATCAT 682
QY 806 AGCGTTTAAAGGAAATTAAGATATCTAATTTATTTAGGAGGTGATTAACAAG 865
Db 683 CAAACTAGTAGAGCTTATTTGAATATATCTGATTTATGCTATATGTTATATCG 742
QY 866 GTTTAATCGAATTAAGACAGCGCGGTCAAGTCTGAAGTTTGGTGAATTTAAT 925
Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTCTACAGCTTGTAGAAATTTCAAT 802
QY 926 TTGATAGAAATGACGTTGGCGTATTTGATATTTATTTGCTATTTTCAACTTAT 985
Db 803 ATGTAGAGAGATGACCTTATGATTTATTTAGATTTAGTACATCAATTTTCAAG 862
QY 986 TTGAAAAATTCATTAGCAACAAGTGTAGATTAATCTAGGAAATTTATACAGAT 1045
Db 863 TTACTATTTACCAATTAAGAAACAGATTTTCAGTTGATAGGTCATTTATACAG 922
QY 1046 TGGGATATTCAAGGGGAAATTAATGTTGGGA 1077
Db 923 TTGTTTGTACATCTGATAGTCTTAGGGGA 954

RESULT 7
US-09-668-650-11
Sequence 11, Application US/09668650
Patent No. 6780408
GENERAL INFORMATION:
APPLICANT: Bosch, Hendrick J.
TITLE OF INVENTION: Stiekema, Willem J.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: No. 6780408artle Corporation
STREET: 3054 Cornwallis Road
City: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668, 650
FILING DATE: 22-SEP-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3726
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-668-650-11

Query Match 8.0%; Score 172.4; DB 3; Length 3726;
Best Local Similarity 54.2%; Pred. No. 5.7e-32;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGAAATCAGCTCCGGATATAGTAACTATTGGGACATACCTTATACAAATCTTGTAGAAC 346
Db 158 GCGATGCAACAAAGAGCAGATATCTATTTGGACAACTAGTCTCTTATACAGCAC 217
QY 347 CCGATATAGTGAATTCCTGTAATATTT-----CAATATTAACAACAACTCAATCCGT 400
Db 218 CTTCTCTTACTGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACAGAGATA 277
QY 401 CTTCTGCTCAATCTGTGACGACCTTTCTATATGATTTAGTATCTAATTTGTAAG 460
Db 278 GTATGGAACATCCATATACAGATTTGTCTATATGACCTTATATCTAATTTGATTTAC 337
QY 461 AGGTAGAGAGACCGTTAATGTAAGTGAACGGGTTGACATTTTGAAGGTGAATAGACGCT 520
Db 338 GGTATAGTCAGAGTGTATTAATTAAGATGGAGATGCAATTTATATGATCTGACTTAT 397
QY 521 ATCAAGATATATATCTTC-----ATTATCTGAGATTTGGCTTAACAGATA 565
Db 398 ACAGAACTATTAGAGGCTCTGATAGCTGAATTAAGATCTTAATCTGCTTCGCTG 457
QY 566 AATCAATCTTAAAACTTGTGACGTAATTAACAGTTCACAGACGGAGAAAGATT 625
Db 458 AAGAACTCCGTACTCGTTTGAATCGCCAGCTCAGAAATTTGATTAATTTAACCCG 517
QY 626 TCACATACTTTTGAAGGCTCATTTATCAAGACAGAAAGCTGAATTTATTTAGCC 685
Db 518 GGTCTTTAAGAAATGGGCTCGTTAGCTAGCAAAAATGCCAAATTTATTTACCT 577
QY 686 CGATGTGCAAGCTGCAGATGTGATTTATTTACTATTTAAGGACGCAATTAATTA 745
Db 578 CTTTTCGAGCGCTGATTTTTCATTTATTTACTTAAGGAGATGCTACTAATATNGCA 637
QY 746 AAGATGGGACTAGTGTGTCCACCGTGTATCCAGGGTCAAGGAGAACTGATTTGAC 805
Db 638 CTAAATGGGGCTATACATGCTACACCTTTTAA-----ATTATCAAT 682
QY 806 AGCGTTTAAAGGAAATTAAGATATCTAATTTATTTAGGAGGTGATTAACAAG 865
Db 683 CAAACTATTAAGCTTATTTAGATATATGATTTATTTGCTATATTTGTAATTCGAG 742
QY 866 GTTTAGATCAGATTAAGACAGCGGGTACAGTCTGAAGTTTGGTGAATTTAATTAAT 925
Db 743 GTTTCACGAACTAAGCAACAGGCACTAGTCTACAGCTTGTGTAATTTCAATAGT 802
QY 926 TTGATAGAAATGACGTTGGCGTATTTGATTTATTTGCTATATTTTCAACTATGAT 985
Db 803 ATGTAGAGAGATGACATTTGATGATTTAGATATGATAGATCAATTTTCAAGCTTGA 862
QY 986 TTGAAAAATTCATTAGCAACAAGTGTAGATTTAATCTAGGAAATTTATACAGAT 1045
Db 863 TTACTAATTTACCAATTAAGAAACAGATTTTCAGTTGATAGGTCATTTATACAGAT 922
QY 1046 TGGGATATTCAAGGGGAAATTAATGTTGGGA 1077

Db 923 TTGGTTTGTACATCGTAGTACTCTTAGGGGA 954

RESULT 8
US-09-661-322A-29
Sequence 29, Application US/09661322A
Patent No. 6593293
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rel
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Ruper, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 2407
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-09-661-322A-29

Query Match 7.6%; Score 162.8; DB 3; Length 2407;
Best Local Similarity 53.4%; Pred. No. 1.1e-29;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;

QY 287 GGGATCAGTCTCGATATAGTAACTATGGACATACCTTATCAATCTTGTAGAAC 346
DB 158 GCGATGAGCAAAAGAGACATCTATGGACACCAATGTCTCTTATCAGAC 217
QY 347 CCGGTATAGGTGGAATCTCTTAATATTT-----CATATATAACAATCTATCCGT 400
DB 218 CTCTCTTACTGATTAATTTCAATAGATATGACCTTATGGTAAAGTACTAGAGGTA 277
QY 401 CTCTGTGCAATCTGTGAGCAGCACTTCTATATGATTTATGATCTATATTTGTAAG 460
DB 278 GTATGTGACATCATATCAGATTTGCTATATATGACTTATCTATATATATTTAC 337
QY 461 AGGTAGCAGAGCGGTATAGTACGCGGTGAGATTTTGAAGGTAATGACTGCT 520
DB 338 GGGTATGACAGAGTGTATTAATATGATGGATTCAGATTTTAATGTTCTGTA 397
QY 521 ATCAAGATATATCTTC-----ATTATCTTGAGATTTGGCTTACAGATA 565
DB 398 ACAGAACTATTTAGAGGCTGTGATAGCTGGAATTAAGAACTTATCTGCTCTG 457
QY 566 AATCAATCTTAAATACTTGTGACGATTAACAGTTCCAGCACGGAGAGAAAT 625
DB 458 AAGAACTCCGTAATCTGTTTGAATCGCCGACTCAGAAATTTGATAGAAATTTA 517
QY 626 TCACTAACTTTTACAGAGGCTTATATCAGACAGAAAGCTGAATATTTATGCTA 685
DB 518 GGTCTTTAAGCAATGAGGCTGCTAGCTAGCAAAATGCCAAATTTATTTACTT 577
QY 686 CGTATGCAAGCTGCAATGCTATTTATCTATTTAAGGACGCGATTAAATATTA 745
DB 578 CTTTTGGAGGCTGCAATTTTCCATTTATTTACTTACAGAGGATGCTACTGATATG 637
QY 746 AAGAAATGGGACTAGTGTGTCACCGTTGATCCAGGGTCAAGGAAAGTATGTAAG 805
DB 638 CTAAATGGGGCTATACAACTACACCTTTATTA-----ATTATCAAT 682
QY 806 AGCGTTAAAGCAAAATTAAGATTAATTAATTTATGTTAGGGTGTATTAACAG 865
DB 683 CAAAACTAGTAGACTTATTAATTAATTAATTTATGTTAGGGTGTATTAACAG 742
QY 866 GTTTAGATCAGTAAAGCAGCGGGTCAAGTGTGTAAGTTGGTCAAAATTTATTAAT 925

Db 743 GTTACACGAATTAAGCAACAGAGGCTTACTAGTACGCTTGTGTAATTTCAATGAT 802
QY 926 TTGTAGAGAAATGACGTTGGCGGTATTTGATTAATTTGCTATATTTCAACTATGAT 985
DB 803 ATCGAGAGAGATGACATTTGATGGGATTTAGAAATAGATCATTTTCAAGTCTGATA 862
QY 986 TTGAAAAATATCCATTAGCAACAGTGTAGATTACTAGGAAATTTATACAGATCCAG 1045
DB 863 TTACTAATTTACCAATGAAACAGATTTTCACTGATGATAGGGTCAATTTATACAGATCCAA 922
QY 1046 TGGATATTTACGGGCAATTTATGTTGGAA 1077
DB 923 TTGGTTTGTACATCGTAGTACTCTTAGGGGA 954

RESULT 9
US-09-661-322A-5
Sequence 5, Application US/09661322A
Patent No. 6593293
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rel
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Ruper, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 1959
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-09-661-322A-5

Query Match 5.6%; Score 119.8; DB 3; Length 1959;
Best Local Similarity 55.0%; Pred. No. 2.8e-19;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;

QY 561 AGATTAATCAATCTTAAATACTTGTGACGATTTAAAGTTCAGACCGGAGAA 620
DB 411 AGATTAACGAAATGATGCAAGATCAAGACATTTCTTGAAGGCTATGTTGTTAGA 470
QY 621 AGATTTCACTAACTTTTACAGAGGCTATTAATCAAGCAGAAAGCTGAATATTTAT 680
DB 471 ACTTGACATTACTACGCTTATACCGCTTTTCAAGAAATCGAAATGAAAGATTCATTA 530
QY 681 GCTTACATGATGCAAGCTCAATGTCATTTATTAATTAAGGACGAGTAAATA 740
DB 531 AATGTATATGCTACAGCTCAAAATTTACACTTATTTATTTAGAGACGATCCCTTT 590
QY 741 TAAAAAAGAAATGGGAACTAGTGTGTCACCGTTGTATCCAGGCTCAGGAGAACTGAT 800
DB 591 TGGTATGTAATGGGAGTGCATCTTCGATGTTAACCA-----TA 632
QY 801 TAAAGAGGCTTAAAGCGAAATTAAGAGCTATCTAATTTATTTAGGGTGTATTA 860
DB 633 TTACACGAAACAAATCAGATATACAGGAATTTTCAACATTTGCTCAATGATATTA 692
QY 861 CAAGGTTTATGATCAGTAAAGCAGGCGGTACAGGCTGAAAGTTGTCGAAATTTAA 920
DB 693 TACAGGCTTAAATTAATCTTAAGA-----GGCAAAATGCTGAAAGTTGTCGCTATTA 746
QY 921 TAAATTTGTAGAGAAATGACGTTGGGATTTAGATTAATTTATTTTCAACTTA 980
DB 747 TCAATTCGTAGAGACCTTAAGTTAGGGGATTAAGATTTAGTACCTATTTCCAACTA 806
QY 981 TGAATTTGAAATATTCATTAACCAACAGTGTAGTTAACTAGGAAATTTATTAACAG 1040
DB 807 TGATACTGCACTTATTCATTAATCAATGAGAGTGTCTGATTAAAGAAATTTATACAG 866

FILING DATE: 07-JUN-1995

2071 1C6A10G0H1A11

||| |||

GENERAL INFORMATION:

APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S. M.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panlitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,046
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-779-046-3

Query Match 5.5%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 8.4e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

QY 561 AGATAAATCAATCTTAAAACTTGTGACGTAGTTAAACAGTTCCAGACGGGAAGA 620
DB 492 AGATAACCGAAATGACAGATCAAGAACATTAATCTTGACGCTATGTCTTAA 551
QY 621 AGATTCACTAACTTTTACAGAGGTATATCAAGACAGAAAGCTGAATATATTT 680
DB 552 ACTTGACATTACTGCTATACCGCTTTTCAGAATTCGAAAGAAAGAACTTCATTAT 611
QY 681 GCCTAGTATGTCAAGCTCAATGTGCAATTTATTTATTTAAGGACGAGTAAATA 740
DB 612 AATGATATATGCTCAAGCTCAATTTACCTATTTATTTAGAGACGCAATCCCTTT 671
QY 741 TAAAAAAGATGGGACTAGTGTGTCACCGTTGTATCCAGGGTCAAGGAGAACTGATTG 800
DB 672 TGGTAGATGGGGGATGCGATCTTCGATGTTAACCA-----TA 713
QY 801 TAACGAGCGGTAAAGCGAAATTAAGCTATACATTAATTTAGTGTAGGTGTATTA 860
DB 714 TTACCAAGAAACAATACATATACAGAGAAATTTTACCAATGCGTACAAATGTATTA 773
QY 861 CAAGGTTTATGATCAGATTAAGACAGCGGGGTACAGTGTGAATTTGTGGAATTTAA 920

DB 774 TACAGGCTAAATTACTTAAG-----CGGCAATCTGAAATGTTGGTCCGATTA 827
QY 921 TAAATTGCTAGAGAAATGACCTTGCGGTATGTAATTTATTTTCCAACTTA 980
DB 828 TCAATTCGCTAGAGACTTAACCTTAGGGTATTAAGTACGCCATTTCCAAAGCTA 887
QY 981 TGAATTTGAAAAATTCCTTACGCAACAGCTAGATTAAGTAAATTTATTAACGA 1040
DB 888 TGAATCTGCACTTATCCATTAATTCAGATGCTCAGTTAACAGAAATTTATTAACGA 947
QY 1041 TCCAGTGGATATTAAGGGGAAATTAATGTTGGAAACGTTTATTTAGCTTAAT 1095
DB 948 TCCATTTGGAGAAACAATGACCTTCAGATTTTCAGATTAAGTATGTTTAAAT 1002

RESULT 14
US-08-881-340-3
Sequence 3, Application US/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panlitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSER: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-881-340-3

Query Match 5.5%; Score 118.2; DB 2; Length 3934;
Best Local Similarity 54.8%; Pred. No. 8.4e-19;
Matches 293; Conservative 0; Mismatches 218; Indels 24; Gaps 2;

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

: FILING DATE: 13-SEPT-1991
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: M/S 102D.C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (904) 375-8100
: TELEFAX: (904) 372-5800
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3684 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
US-08-448-170-7

```

Query Match	5.4%;	Score 116.8;	DB 2;	Length 3684;	
Best Local Similarity	55.0%;	Pred. No. 1.8e-18;			
Matches 310;	Conservative	0;	Mismatches 227;	Indels 27;	
				Gaps 3	
Qy	532	TATCTTCATTA	TCCTTGAGATTGGCTTACAGATAAATCAATTCCTAA	AAAACTTGCTAC 591	
Db	400	TATCAACGTCAC	TTTGAAGATTGGCTAGAAAACCGTGA	TGTAAGAACGAAAGTCTT 459	
Qy	592	GTA	CTTAAACGTTCCAAACGGGAAAGAAATTTCACTTAACTTTT	AGCAGGCTATTA 651	
Db	460	CTTATATCCCA	TATATATAGCCTTAGAACTTGAACTTTTCTTAA	TGCAATGCCCTTTTCGA 519	
Qy	652	TCAGA	CAGAAAGCTGAAATATTTATATATGCTCTAGTATGCAAGCTGCAATATG	CGAT 711	
Db	520	ATTGAA	AAACCAAGAGTTCATTTATATG---GTA	TATGCTCAAGCTGCMAATTTACAC 576	
Qy	712	TTATTA	CTATTAAAGGACGCA	GTTAAATATMAAAGAATGAGGACTATGATGCCACCG 771	
Db	577	CTATTA	TATATGAAGATGCTCTCTTTTGGTATGTAATTTGGGCTTAC	TCCCAAGAA 636	
Qy	772	TTGAT	CCAGGCTCAGGGAGAACTGTTGTACAGAGCGGTTAA	AAAGCAAAATTAAGAG 831	
Db	637	ATTCA	AG-----TTAT	TATAGGCCCAAGTGGA	AAAAACGAGAA 678
Qy	832	TATAC	TATATTTGTTAGGCTGATATACAAAGGCTT	TAGATCAGATPACAGAGCGGT 891	
Db	679	TATCT	GATTATTCGCAAGATGTTATATATACGGGTTTAA	TATTTGAGA-----GGG 732	
Qy	892	ACA	AGTCTGAAGTTTGGTGC	AAATTTATATTAATTTGTATAGAAATGACGTTGGCGGTA 951	
Db	733	ACA	ATCTGTAAGTTGGTGC	ATATATCAATTTCCGTATGAGACTTAAACGCTTGAGTA 792	
Qy	952	TTGAT	ATTTATGCTATATTTCCAACTTATGATTTTG	AAAAATATCACTTATGCAACAGT 1011	
Db	793	TTA	ATCTAGTGGC	ACTATTTCCCAAGCTATACACGGGTGTTTATCCAA	TATATACAGT 852
Qy	1012	GTA	GATTTAACTAGGAAATTTATACAGATTC	ACAGTGGGATATTCAGGGGGAATTAATGTT 1071	
Db	853	GCTCA	ATTTAACAGAGAAATTTATACAGATTC	CAATTTGGGAGAAACAATATGCACTTCAGGA 912	
Qy	1072	TGG	AAGGTTTTTTTACCTTAA	T 1095	
Db	913	TTT	GCAAGTACGAATTTGTTTAA	T 936	

Search completed: December 19, 2005, 13:03:16
Job time : 273.352 secs

This page is empty

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:54:29 ; Search time 200.901 Seconds
(without alignments)
5233.604 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataataatgctt.....atagttattatcaaltta 2145

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA-New:*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB_seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB_seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq.*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB_seq.*
5: /cgn2_6/ptodata/1/pubpna/PCr_NEW_PUB_seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB_seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	4.9	1860	US-11-058-727-15	Sequence 15, Appl
2	105	4.9	1860	US-11-108-389-15	Sequence 15, Appl
3	105	4.9	2010	US-11-058-727-11	Sequence 11, Appl
4	105	4.9	2010	US-11-108-389-11	Sequence 11, Appl
5	105	4.9	3621	US-11-058-727-1	Sequence 1, Appl
6	105	4.9	3621	US-11-108-389-1	Sequence 1, Appl
7	105	4.9	4874	US-11-058-727-17	Sequence 17, Appl
8	105	4.9	4874	US-11-108-389-17	Sequence 17, Appl
9	101.8	4.7	2019	US-11-058-727-55	Sequence 55, Appl
10	101.8	4.7	2019	US-11-058-727-87	Sequence 87, Appl
11	101.8	4.7	2019	US-11-108-389-55	Sequence 55, Appl
12	101.8	4.7	2019	US-11-108-389-87	Sequence 87, Appl
13	100.2	4.7	2019	US-11-058-727-59	Sequence 59, Appl
14	100.2	4.7	2019	US-11-058-727-91	Sequence 91, Appl
15	100.2	4.7	2019	US-11-108-389-59	Sequence 59, Appl
16	100.2	4.7	2019	US-11-108-389-91	Sequence 91, Appl
17	99.4	4.6	4359	US-11-091-643-3	Sequence 3, Appl
18	98.6	4.6	1863	US-11-058-727-19	Sequence 19, Appl
19	98.6	4.6	1863	US-11-108-389-19	Sequence 19, Appl
20	98.6	4.6	2019	US-11-058-727-57	Sequence 57, Appl
21	98.6	4.6	2019	US-11-058-727-89	Sequence 89, Appl
22	98.6	4.6	2019	US-11-108-389-57	Sequence 57, Appl
23	98.6	4.6	2019	US-11-108-389-89	Sequence 89, Appl

24	98.6	4.6	2022	7	US-11-058-727-7	Sequence 7, Appl
25	98.6	4.6	2022	7	US-11-058-727-21	Sequence 21, Appl
26	98.6	4.6	2022	7	US-11-058-727-25	Sequence 25, Appl
27	98.6	4.6	2022	7	US-11-058-727-29	Sequence 29, Appl
28	98.6	4.6	2022	7	US-11-058-727-33	Sequence 33, Appl
29	98.6	4.6	2022	7	US-11-058-727-43	Sequence 43, Appl
30	98.6	4.6	2022	7	US-11-058-727-49	Sequence 49, Appl
31	98.6	4.6	2022	7	US-11-058-727-67	Sequence 67, Appl
32	98.6	4.6	2022	7	US-11-058-727-69	Sequence 69, Appl
33	98.6	4.6	2022	7	US-11-058-727-75	Sequence 75, Appl
34	98.6	4.6	2022	7	US-11-058-727-81	Sequence 81, Appl
35	98.6	4.6	2022	7	US-11-108-389-7	Sequence 7, Appl
36	98.6	4.6	2022	7	US-11-108-389-21	Sequence 21, Appl
37	98.6	4.6	2022	7	US-11-108-389-25	Sequence 25, Appl
38	98.6	4.6	2022	7	US-11-108-389-29	Sequence 29, Appl
39	98.6	4.6	2022	7	US-11-108-389-33	Sequence 33, Appl
40	98.6	4.6	2022	7	US-11-108-389-43	Sequence 43, Appl
41	98.6	4.6	2022	7	US-11-108-389-49	Sequence 49, Appl
42	98.6	4.6	2022	7	US-11-108-389-67	Sequence 67, Appl
43	98.6	4.6	2022	7	US-11-108-389-69	Sequence 69, Appl
44	98.6	4.6	2022	7	US-11-108-389-75	Sequence 75, Appl
45	98.6	4.6	2022	7	US-11-108-389-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-11-058-727-15
Sequence 15, Application US/11058727
Publication No. US20050261483A1

GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flanagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: 49PVD
US-11-058-727-15

Query Match 4.9%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 1,4e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;
421 GCACCTTCATATGATGATTTAGTATCTATTAATTCGTAAGAGTACGACGACGCTTTA 480

```
Db 205 GAAATTTTATGACACAGTAGAAGAACTCATTAATCAAAAAATAGACAGATATGACAGG 264
QY 481 AGTACGGGGTGCAGATTTTGGAGGTGAATGACGCTTATCAAGATTATTTCTTCAT 540
Db 265 AATTAAGCGCTTTCGGAATTAGAAGATTAGTATATTAACA---TTATATCTTAAT 321
QY 541 TATCTTGAGATTGGCTTACAGATTAATCAAAATCTTAAAAAACTTGCTGACGTAGTAA 600
Db 322 GCGCTTGAAGATGGGAGAAAATCCAAATGTTCAAGACCTTACAGAGATGCGCAAT 381
QY 601 CAGTTCCAGACCGGAGAGAAATTTCACTTAACCTTTAGCAGGCTATTAACAAGACAG 660
Db 382 CGATTGAAATCTGTAGTATTTATCCCAATATATGCCA---TCTTTAGAGTGACA 438
QY 661 AAAGCTGAATATTAATATGCTACGTATGTAAGCTGCAAAATGTCATTAATTA 720
Db 439 AATTTGAAGTACATTCCTTACTGATATGCAATGACAGCCAACTTACTTACTGTA 498
QY 721 TTAAGGACCGCAGTAAATTAATAAAAAAGAAATGGGAGCTAGTGTGCCACCGTTGATCCA 780
Db 499 TTAAGGACCGCAGTAAATTTTGGAGAAATGGGA-----TGGTCA 540
QY 781 GGGTCAGGAGAACTGATTTGTAACGACGGTTAAAGCGAAAATAAAGATTAAT 840
Db 541 ACAACTACTATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 841 TATGTGTAGGATGATTAACAAGGCTTATGATGATGATGATGATGATGATGATGATGAT 900
Db 601 CACTGTGTAAGTGTATGAACTGTTTACGAAATTTAAA-----GGCAGAGGCT 654
QY 901 GAAATTGTCGAAATTTAAATAATTTGATGAGAAATGACGTTGGCGGTATTTGATTT 960
Db 655 AAACAATGGGTGACATTAACAATTCGATGAGAAATGACACGCGGTTTAAATGTT 714
QY 961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCATTAACACAGTGTAGGTTA 1020
Db 715 GTTGCAATTAATCCCAATTAATGACACAGCAGTACCAATGGAAGCAACAATA 774
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
Db 775 ACAAGGAAATTAATACAGATCCAGTGGG 803

RESULT 2
; Sequence 15, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
```

```
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15

Query Match 4.9%; Score 105; DB 7; Length 1860;
Best Local Similarity 53.1%; Pred. No. 1.4e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACCTTCAATATGATTTAGTATCTATTAATTCGTAAGAGGTGACGAGCGGTGA 480
Db 205 GAAATTTTATGACACAGTAGAAGAACTCATTAATCAAAAAATAGACAGATATGACAGG 264
QY 481 AGTACGGGGTGCAGATTTTGGAGGTGAATGACGCTTATCAAGATTATTTCTTCAT 540
Db 265 AATTAAGCGCTTTCGGAATTAGAAGATTAGTATATTAACA---TTATATCTTAAT 321
QY 541 TATCTTGAGATTGGCTTACAGATTAATCAAAATCTTAAAAAACTTGCTGACGTAGTAA 600
Db 322 GCGCTTGAAGATGGGAGAAAATCCAAATGTTCAAGACCTTACAGAGATGCGCAAT 381
QY 601 CAGTTCCAGACCGGAGAGAAATTTCACTTAACCTTTAGCAGGCTATTAACAAGACAG 660
Db 382 CGATTGAAATCTGTAGTATTTATTTACGCAATATATGCCA---TCTTTAGAGTGACA 438
QY 661 AAAGCTGAATATTAATATGCTACGTATGTAAGCTGCAAAATGTCATTAATTA 720
Db 439 AATTTGAAGTACATTCCTTACTGATATGCAATGACAGCCAACTTACTTACTGTA 498
QY 721 TTAAGGACCGCAGTAAATTAATAAAGAAATGGGAGCTAGTGTGCCACCGTTGATCCA 780
Db 499 TTAAGGACCGCTCAATTTTGGAGAAATGGGA-----TGGTCA 540
QY 781 GGGTCAGGAGAACTGATTTGTAACGACGGTTAAAGCGAAAATAAAGATTAAT 840
Db 541 ACAACTACTATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 841 TATGTGTAGGATGATTAACAAGGCTTATGATGATGATGATGATGATGATGATGATGAT 900
Db 601 CACTGTGTAAGTGTATGAACTGTTTACGAAATTTAAA-----GGCAGAGGCT 654
QY 901 GAAATTGTCGAAATTTAAATAATTTGATGAGAAATGACGTTGGCGGTATTTGATTT 960
Db 655 AAACAATGGGTGACATTAACAATTCGATGAGAAATGACACGCGGTTTAAATGTT 714
QY 961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCCATTAACACAGTGTAGGTTA 1020
Db 715 GTTGCAATTAATCCCAATTAATGACACAGCAGTACCAATGGAAGCAACAATA 774
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
Db 775 ACAAGGAAATTAATACAGATCCAGTGGG 803

RESULT 3
US-11-058-727-11
; Sequence 11, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
```

```

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-058-727-11

Query Match      4.9%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 1.5e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACCTTCTATATGATTTAGTATCTATATCTTATATGTAAGAGGTAAGAGCGAGCGTGT 480
DB 337 GAATTTTATGGAACAGTGAAGAACTCATTAATAAAAAAGAGATATGCAAG 396
QY 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGACCTGCTTATCAAGATTATCTTCAT 540
DB 397 AATTAAGCGCTTCGGAATTAAGAGATTAAGTATATTAATCAAA--TTATATCTACT 453
QY 541 TATCTTGAGGATTTGGCTTACAGATTAATCAATCTTAAAAAAGCTTGCAAGTATTA 600
DB 454 GCGCTTGAAAGATGGGAAGAAATCCAAATGCTTCAAGAGCTTACAGAGATGCGCAAT 513
QY 601 CAGTTCACAGCAGGGAAGAGATTTCACTAACTTTAGCAGGCTATTATCAAGACAG 660
DB 514 CGATTTGAAATCCGTGATAGTATTATTAACCAATATATGCA--TCCTTTAGAGTGACA 570
QY 661 AAAGCTGAATATATATATGCTACGATATGTCAGACCTGCAATGCAATTTATCTA 720
DB 571 AATTTTAAGTACATTCCTTACTGTAATGCAATGCGACGCACTTCAATTTACTGTTA 630
QY 721 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGAAGTATGTCACCGTTGTATCA 780
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAAGATGGGGA-----TGGTCA 672
QY 781 GGGTCAGGGAAGTATGTAACGACGCGTTAAAGCCGAAATTAAGAGTATCTAAT 840
DB 673 ACAACTACTATTAATTAATCTATATGATGTCGCAATGAACCTTACTGCAAGATATTTGAT 732
QY 841 TATTTGTAGGAGTATTAACAAGGTTTATGATCAGATTAAGACAGGGGGTATCAAGCT 900
DB 733 CACTGTAAGAGTATGTAAGAACTGCTTTAGCAAAATTAATA-----GGCAGAGGCT 786
QY 901 GAAATTTGTCGAATTTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATAT 960
DB 787 AAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACACTGGGGGTTTATAGATTT 846
QY 961 AATGCTATTTTCCAACTTATGATTTTGAAGAAATATCATTAAGCAACAAGTATGATTA 1020
DB 847 GTTGCAATTAATTTCCAAATTAATGACACGCACTGACCAATGAAAGAAAGCAACTA 906
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 907 ACAAGGGAAGTATATACAGATCCAGTGGG 935
```

```

RESULT 4
US-11-108-389-11
; Sequence 11, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Hermann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-11-108-389-11

Query Match      4.9%; Score 105; DB 7; Length 2010;
Best Local Similarity 53.1%; Pred. No. 1.5e-15;
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

QY 421 GCACCTTCTATATGATTTAGTATCTATATCTTATATGTAAGAGGTAAGAGCGGTTA 480
DB 337 GAATTTTATGGAACAGTGAAGAACTCATTAATCAAAATTAAGAGATATGCAAG 396
QY 481 AGTACGGGGTTCAGATTTTGGAGGTGAATGACCTGCTTATCAAGATTATCTTCAT 540
DB 397 AATTAAGCGCTTCGGAATTAAGAGATTAAGTATATTAATTAATCAAA--TTATATCTACT 453
QY 541 TATCTTGAGGATTTGGCTTACAGATTAATCAATCTTAAAAAAGCTTGCAAGTATTA 600
DB 454 GCGCTTGAAAGATGGGAAGAAATCCAAATGCTTCAAGAGCTTACAGAGATGCGCAAT 513
QY 601 CAGTTCACAGCAGGGAAGAGATTTCACTAACTTTAGCAGGCTATTATCAAGACAG 660
DB 514 CGATTTGAAATCCGTGATAGTATTATTAACCAATATATGCA--TCCTTTAGAGTGACA 570
QY 661 AAAGCTGAATATATATATGCTACGATATGTCAGACCTGCAATGCAATTTATCTA 720
DB 571 AATTTTAAGTACATTCCTTACTGTAATGCAATGCGACGCACTTCAATTTACTGTTA 630
QY 721 TTAAGGAGCGCACTTAATATTAATAAAGAAATGGGGAAGTATGTCACCGTTGTATCA 780
DB 631 TTAAGGAGCGCGTCAATTTTGGAGAAAGATGGGGA-----TGGTCA 672
QY 781 GGGTCAGGGAAGTATGTAACGACGCGTTAAAGCCGAAATTAAGAGTATCTAAT 840
DB 673 ACAACTACTATTAATTAATCTATATGATGTCGCAATGAACCTTACTGCAAGATATTTGAT 732
```

OY	841	TATTGTGAGGGTGTGATTAACAAGGGTTTAATCGATTAAGACAGCGGGGTACAAGTCT	900
Db	733	CACGTGTGAAAGTGGTAAAGAACTGGTTTACAAATTTAAAA-----GGCACGAGCGCT	786
OY	901	GAAGTTTGGTGCAAATTTAATTAATTTTGTAGAGAAATGACGTTGGCGGTATTGGATTT	960
Db	787	AAACCAATGGGTGACTATTATACCAAATTCGGTAGAGAAATGACACTGGCGTTTTAGATGTT	846
OY	961	ATTGCTATTATTTCCACACTTATGATTTTGAATAATATTCATTAGCAACAAGGTAGACTTA	1020
Db	847	GTTCGATTATTTCCCAAAATTTATGACACACGACGTACCCAAATGAAACGAAACCAACTA	906
OY	1021	ACTAGGAAATTTATACAGATCCACTGGG	1049
Db	907	ACAAAGGAAGTATATACAGATCCACTGGG	935
RESULT 5			
US-11-058-727-1			
; Sequence 1, Application US/11058727			
; Publication No. US20050261483A1			
; GENERAL INFORMATION:			
; APPLICANT: Andre R. Abad			
; APPLICANT: Ronald D. Flannagan			
; APPLICANT: Rafael Herrmann			
; APPLICANT: Theodore W. Kahn			
; APPLICANT: Albert L. Lu			
; APPLICANT: Billy Fred McCutchen			
; APPLICANT: James K. Presnall			
; APPLICANT: James F.H. Wong			
; APPLICANT: Cao-Guo Yu			
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal			
; TITLE OF INVENTION: Activity			
; FILE REFERENCE: 35718/287809			
; CURRENT APPLICATION NUMBER: US/11/058,727			
; CURRENT FILING DATE: 2005-02-15			
; PRIOR APPLICATION NUMBER: 60/391,786			
; PRIOR FILING DATE: 2002-06-26			
; PRIOR APPLICATION NUMBER: 60/460,787			
; PRIOR FILING DATE: 2003-04-04			
; PRIOR APPLICATION NUMBER: 10/606,320			
; PRIOR FILING DATE: 2003-06-25			
; NUMBER OF SEQ ID NOS: 134			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 3621			
; TYPE: DNA			
; ORGANISM: Bacillus thuringiensis			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(3621)			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (0)...(0)			
; OTHER INFORMATION: CRY1218-1			
US-11-058-727-1			
Query Match 4.9%; Score 105; DB 7; Length 3621;			
Best Local Similarity 53.1%; Pred.No.1.9e-15;			
Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 44			

```

OY 601 CAGTTCACAGCAGCGGAGAAAGANTTCACTAAACTTTTGAACAGGGCTCATTTACAAAGAC 660
DB 514 CGATTGTGAATTCCTGGATAGTTTATTTACGCAATATATGCCA---TCCTTTAGAGTGACA 570
OY 661 AAAGCTGAATATATTTATTTATTCGCTACGATATGTGCAAGCTGCAATGTGATTTATTACTA 720
DB 571 AATTTTGAAGTACCACTTCTTACTGATATATGCAATGGCAGCCACCTTCATTACTGTTA 630
OY 721 TTAAGGACGCAAGTTAAATATATAAAGAAATGGGCACTAGTGTTCACCGTTGTATCCA 780
DB 631 TTAAAGACCGGTCAATTTTGGAGAAAGATGGGGA-----TGGTCA 672
OY 781 GGGTCAGGGAACACTGATTGTATACGACGGCTTTAAAGCGAAATATTAAGATATACTAAT 840
DB 673 ACAACTACTATTAATTAACCTATATATATGATCGTCAAAAGAAACTTACTGCAAAATATCTGAT 732
OY 841 TATGTGTAGGAGTGTATATACAAAGGTTTGAATCATATTAAGACAGGCGGGTACAAGTGT 900
DB 733 CACTGTGTAAGTGTATGAAACTGTGTTTGAACAAATTTAAAA-----GGCAGAGCGCT 786
OY 901 GAAGTTTGTGCAAAATTTAATAAATTTGTAAGAAATGACGTTGCGGTATTTGATATT 960
DB 787 AAACAATGGTGTACTATATACCAATTCGTAGAGAAATGACACTGGCGGTTTAAATGTT 846
OY 961 ATTGTATATTTTCCAACTTATGATTTTGAAAAATATCCATTATGCAACAAGTAAAGTTA 102
DB 847 GTTGATTAATTTCCCAAATTTATGACACAGCAGTACCAATGAAACGAAACACAACTA 906
OY 1021 ACTAGGGAATTTATATACAGATCCAGTGGG 1049
DB 907 ACAAGGGAAGTATATATACAGATCCACTGGG 935

RESULT 6
US-11-108-389-1
; Sequence 1, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108.389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CRY1218-1
US-11-108-389-1

```

Query Match 4.9%; Score 105; DB 7; Length 3621;
 Best Local Similarity 53.1%; Pred. No. 1.9e-15;
 Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

```

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTAAGAGGAGACGAGCGTGT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 337 GAAATTTTATGCAACAGTAGAAGAACTCATTAATCAAAAATAGACATATGCAAG 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 AGTGACGGGGTTGCAATTTTGAGGGTGAATGACCTGCTTACAGATTTATCTTCAT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 AATTAAGCGCTTCGGAATTAGAAGATTTAGATTAATTAACCA---TATATCTACT 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 TATCTTGAGATTTGCTTACAGATAATCAAATCTTAATAAACTTGCTGACGTATTA 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 454 GCGCTTGCAAGATTTGGAAGAAATCCAAATGCTTCAAGACCTTACAGATGTGCAAT 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 CAGTTCCAGACGGGGAAGAAATTTCACTTAACTTTACAGGCTCATATCAAGCAG 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 514 CGATTTGAAATCTGGATAGTTTATTTACGCAATATATGCCA---TCTTTAGAGTGACA 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 AAAGCTGAATATATTTATTTGCTACGTATGTGCAAGCTGCAATGTGATTTATCTA 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 571 AATTTTGAAGTACCATTCCTTACTGTATATGCAATGCGACCACTTCACTTACTGTTA 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 TTAAGGACGCAAGTTAAATATTAATAAAAGAAATGGGCACTAGTGTGCCAGCTGTATCA 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 631 TTAAGGACGCGTCAATTTTGTGAGAGAAATGGGCA-----TGGTCA 672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 GGGTCAGGAGAACTGATTTGTACAGAGCGTTAAACGAAATTAAGAATATCTAT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 673 ACAACTATCTATTAATCTATTTATGATCGTCAATGAACTTCTGCAATATTTCTGAT 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TATTTGTAGGGTGTGTAACAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTCT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 733 CACTGTGTAAAGTGTATGAACTGTTTACCAAAATTTAAA-----GGCAGAGCGCT 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 GAACTTGTGCGAAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATTTGATAT 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 787 AAACAATGGGTGACATTAACCAATTCGTAGAGAAATGACATGGGCGTTTATGATGTT 846
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 ATTGCTATATTTCCACTTATGATTTGAAAAATATCTATTAGCAACAGTGTAGATTA 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 847 GTTGCACTATTTCCCAATTTATGACACACGACGTAACCAATGAAAGAAAGCAACTA 906
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 ACTAGGAAATTTATACAGATCCAGTGG 1049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 907 ACAAGGAAATTTATACAGATCCAGTGG 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 7
 US-11-058-727-17
 ; Sequence 17, Application US/11058727
 ; Publication No. US20050261483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Rafael Herrmann
 ; APPLICANT: Theodore W. Kahn
 ; APPLICANT: Albert L. Lu
 ; APPLICANT: Billy Fred McCutchen
 ; APPLICANT: James K. Presnail
 ; APPLICANT: James F.H. Wong
 ; APPLICANT: Cao-Guo Yu
 ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
 ; TITLE OR INVENTION: Activity
 ; FILE REFERENCE: 35718/287809
 ; CURRENT APPLICATION NUMBER: US/11/058.727
 ; PRIOR FILING DATE: 2005-02-15
 ; PRIOR APPLICATION NUMBER: 60/391,786
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: 60/460,787
 ; PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 4874

TYPE: DNA

ORGANISM: Bacillus thuringiensis

FEATURE:

NAME/KEY: misc feature

LOCATION: (0) - (0)

OTHER INFORMATION: Genomic DNA 1218-1

US-11-058-727-17

Query Match 4.9%; Score 105; DB 7; Length 4874;
 Best Local Similarity 53.1%; Pred. No. 2.2e-15;
 Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

```

QY 421 GCACTTCTATATGATTTAGTATCTATATCTGTAAGAGGAGACGAGCGTGT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1067 GAAATTTTATGCAACAGTAGAAGAACTCATTAATCAAAAATAGACATATGCAAG 1126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 AGTGACGGGGTTGCAATTTTGAGGGTGAATGACCTGCTTACAGATTTATCTTCAT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1127 AATTAAGCGCTTCGGAATTAGAAGATTTAGATTAATTAACCA---TATATCTACT 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 TATCTTGAGATTTGCTTACAGATAATCAAATCTTAATAAACTTGCTGACGTATTA 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1184 GCGCTTGAAATATGGAAGAAATCCAAATGTTCAAGACCTTACAGATGTGCAAT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 CAGTTCCAGACGGGGAAGAAATTTCACTTAACTTTAGCAGGCTCATATCAAGCAG 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1244 CGATTTGAAATCTGGATAGTTTATTTACGCAATATATGCCA---TCTTTAGAGTGACA 1300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 AAAGCTGAATATATTTATTTGCTACGTATGTGCAAGCTGCAATGTGATTTATCTA 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1301 AATTTTGAAGTACCATTCCTTACTGTATATGCAATGCGACCACTTCACTTACTGTTA 1360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 TTAAGGACGCAAGTTAATAATTAATAAAAGAAATGGGCACTAGTGTGCCAGCTGTATCA 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1361 TTAAGGACGCGTCAATTTTGTGAGAAATGGGCA-----TGGTCA 1402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 GGGTCAGGAGAACTGATTTGTACAGAGCGTTAAACGAAATTAAGAATATCTAT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1403 ACAACTATCTATTAATCTATTTATGATCGTCAATGAACTTCTGCAATATTTCTGAT 1462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TATTTGTAGGGTGTGTAACAAGGTTTATGATCAGATTAAGACAGCGGGTACAGTCT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1463 CACTGTGTAAAGTGTATGAACTGTTTACCAAAATTTAAA-----GGCAGAGCGCT 1516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 GAACTTGTGCGAAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATTTGATAT 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1517 AAACAATGGGTGACATTAACCAATTCGTAGAGAAATGACATGGGCGTTTATGATGTT 1576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 ATTGCTATATTTCCACTTATGATTTGAAAAATATCTATTAGCAACAGTGTAGATTA 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1577 GTTGCACTATTTCCCAATTTATGACACACGACGTAACCAATGAAAGAAAGCAACTA 1536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 ACTAGGAAATTTATACAGATCCAGTGG 1049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1637 ACAAGGAAATTTATACAGATCCAGTGG 1665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 8
 US-11-108-389-17
 ; Sequence 17, Application US/11108389
 ; Publication No. US20050261188A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Rafael Herrmann
 ; APPLICANT: Theodore W. Kahn
 ; APPLICANT: Albert L. Lu

```
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ CURRENT FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 4874
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17
```

Query Match 4.9%; Score 105; DB 7; Length 4874;

Best Local Similarity 53.1%; Pred. No. 2.2e-15; Matches 334; Conservative 0; Mismatches 265; Indels 30; Gaps 4;

```
QY 421 GCACTTCTATATGATGATTAATCTATTAATCGTAAAGAGTAGAGACGGTGT 480
DB 1067 GAAATTTTATGACAGTAGAGAACTCATTAATCAAAAATAGCAAGATTGCAAG 1126
QY 481 AGTAGCGGGTTGCGAATTTTGGAGGTGAATGACGCTTATCAAGATTATCTTCAT 540
DB 1127 AATTAAGCGCTTCGGAATTAGAAGATAGATTAATATTAACAA---TTATATCTAAGT 1183
QY 541 TATCTTGAGATTTGGCTTACAGATTAATCAATCTTAAATCTTGCTGACGATGTTAA 600
DB 1184 GCGCTTGAAAGAAATGGAGAAATCCAAATGGTTCAAGACCTTACAGATGTGCAAAAT 1243
QY 601 CAGTTCGAAGCAGGAGAAAGATTTCATCTTAACTTTACAGGGTCATTATCAAGCAG 660
DB 1244 CGATTTGAATCTCGATTAATTTTACCAATATATGCCA---TCTTTAAGTGACA 1300
QY 661 AAAGCTGAATATATATATGCTAGCTATGTGCAAGCTGCAATGTGCAATTTACTA 720
DB 1301 AATTTGAAGTACATTCCTTACTGTATATGCAATGGCAGCAACCTTCACTTACTGTTA 1360
QY 721 TTAAGGAGCGCAATTAATATAAAAAAGATGGGAGCTAGTGTGCCAGCTGTATCCA 780
DB 1361 TTAAAGACCGCTCAATTTTGGAGAAATGGGGA-----TGGTCA 1402
QY 781 GGGTCAGGAGAACTGATTTGTAAAGCGGTTAAAGCGAAATTAAGAGTATACAT 840
DB 1403 ACAACTACTATTAATTAATTAATGATCGTAAATGAACTTCTGCAAGATATTCGAT 1462
QY 841 TATTTGTAGGTTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTACAGTGT 900
DB 1463 CACTGTGTAAGTGTATGAACTGGTTTACGAAATTAATAA-----GGCAGAGCGCT 1516
QY 901 GAAGTTTGTGCAAAATTAATAATTTCTAGAGAAATGACGTTGGCGGTATTTGATATT 960
DB 1517 AAACAAATGGGTGATCATTAACCAATTCCTAGAGAAATGACACTGGCGGTTTAAAGTGT 1576
QY 961 ATTGCTAATTTTCAACTTATGATTTTGAATAATATCATTAACAACAGTATGAGTTA 1020
DB 1577 GTTGCAATATTTCCAAATTTATGACACGCACTGACCAATGGAAGAAAGCAACTA 1636
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
```

DB 1637 ACAAGGAAGTATATACAGATCCAGTGGG 1665

RESULT 9

US-11-058-727-55

/ Sequence 55, Application US/11058727

/ Publication No. US20050261483A1

/ GENERAL INFORMATION:

/ APPLICANT: Andre R. Abad

/ APPLICANT: Ronald D. Flannagan

/ APPLICANT: Rafael Herrmann

/ APPLICANT: Theodore W. Kahn

/ APPLICANT: Albert L. Lu

/ APPLICANT: Billy Fred McCutchen

/ APPLICANT: James K. Presnall

/ APPLICANT: James F.H. Wong

/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal

/ FILE REFERENCE: 35718/287809

/ CURRENT APPLICATION NUMBER: US/11/058,727

/ PRIOR FILING DATE: 2005-02-15

/ PRIOR APPLICATION NUMBER: 60/391,786

/ PRIOR FILING DATE: 2002-06-26

/ PRIOR APPLICATION NUMBER: 60/460,787

/ PRIOR FILING DATE: 2003-04-04

/ PRIOR APPLICATION NUMBER: 10/606,320

/ PRIOR FILING DATE: 2003-06-25

/ NUMBER OF SEQ ID NOS: 134

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 55

/ LENGTH: 2019

/ TYPE: DNA

/ ORGANISM: Bacillus thuringiensis (mutated)

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)...(2019)

US-11-058-727-55

Query Match 4.7%; Score 101.8; DB 7; Length 2019;

Best Local Similarity 58.6%; Pred. No. 8.6e-15; Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

```
QY 661 AAAGCTGAATTTATATATGCTTACGATATGCAAGCTGCAAAATGTCATTATTA 720
DB 583 AATTTGAAGTACATTCCTTACTGTATATGCAATGGCAGCAACCTTCACTTACTGTTA 642
QY 721 TTAAGGAGCGCAATTAATATAAAAAAGATGGGAGCTAGTGTGCCAGCTGTATCCA 780
DB 643 TTAAGGAGCGCTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 781 GGGTCAGGAGAACTGATTTGTAAAGCGGTTAAAGCGAAATTAAGAGTATACAT 840
DB 685 ACAACTACTATTAATTAATTAATGATCGTCAAAATGAACTTCTGCAAGATATTCGAT 744
QY 841 TATTTGTAGGTTGATTAACAAGGTTTATGATCAGATTAAGACAGCGGTTCAAGTGT 900
DB 745 CACTGTGTAAGTGTATGAACTGGTTTACGAAATTAATAA-----GGCAGAGCGCT 798
QY 901 GAAGTTTGTGCAAAATTAATAATTTCTAGAGAAATGACGTTGGCGGTATTTGATATT 960
DB 799 AAACAAATGGGTGATCATTAACCAATTCCTAGAGAAATGACACTGGCGGTTTAAAGTGT 858
QY 961 ATTGCTAATTTTCAACTTATGATTTTGAATAATATCATTAACAACAGTATGAGTTA 1020
DB 859 GTTGCAATATTTCCAAATTTATGACACGCACTGACCAATGGAAGAAAGCAACTA 918
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 919 ACAAGGAAGTATATACAGATCCAGTGGG 947
```

RESULT 10

US-11-058-727-87
; Sequence 87, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis* (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-87

Query Match 4.7%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 8.6e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

QY 661 AAAGCTGAATATATTATTTGCTTACGTATGTCAGCAAGCTGCAATGTGATTTATCTA 720
DB 583 AATTTGAAGTACATTCCTTACTGTATATGCAATGCAAGCACAACCTTACTTTACTGTTA 642
QY 721 TTAAAGGACGCACTTAATATTAATAAAGAAATGGGACTAGTGTGTCCACGGTGTATCCA 780
DB 643 TTTAAAGACCGCGCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATATCTAAT 840
DB 685 ACAACTACTATTTATTAATCTATTTATGATGTCAAATGAACTTACTGCAATATTTCTGAT 744
QY 841 TATTTGTAGCGGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGTACAAGTCT 900
DB 745 CACTGTATAAGTGTATGAACTGTTTGGCAAAATTAATA-----GGCAGAGCGCT 798
QY 901 GAAGTTTGTGCAAAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATT 960
DB 799 AAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACACTGGCGGTTTATGATGTT 858
QY 961 ATTGCTATATTTTCCAAATTTATGATTTGAAATAATATCCATTAGCAACAAGTATGATTA 1020
DB 859 GTTGCAATATTTCCCAATTTATGACAAATTAACGTAACCAATAGAAAGAAAGCAACTA 918
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 919 ACAAGGAAGTATATACAGATCCAGTGGG 947

RESULT 11
US-11-108-389-55
; Sequence 55, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:

APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
PRIOR FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 2019
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-11-108-389-55

Query Match 4.7%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 8.6e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;

QY 661 AAAGCTGAATATATTATTTGCTTACGTATGTCAGCAAGCTGCAATGTGATTTATCTA 720
DB 583 AATTTGAAGTACATTCCTTACTGTATATGCAATGCAAGCACAACCTTACTTTACTGTTA 642
QY 721 TTAAAGGACGCACTTAATATTAATAAAGAAATGGGACTAGTGTGTCCACGGTGTATCCA 780
DB 643 TTTAAAGACCGCGCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTTAAAGCGAAATTAAGATATCTAAT 840
DB 685 ACAACTACTATTTATTAATCTATTTATGATGTCAAATGAACTTACTGCAATATTTCTGAT 744
QY 841 TATTTGTAGCGGTGTATTAACAAGGTTTAGATCAGATTAAGACAGCGGGTACAAGTCT 900
DB 745 CACTGTATAAGTGTATGAACTGTTTGGCAAAATTAATA-----GGCAGAGCGCT 798
QY 901 GAAGTTTGTGCAAAATTTAATAATTTGTAAGAAATGACGTTGGCGGTATTTGATATT 960
DB 799 AAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACACTGGCGGTTTATGATGTT 858
QY 961 ATTGCTATATTTTCCAAATTTATGATTTGAAATAATATCCATTAGCAACAAGTATGATTA 1020
DB 859 GTTGCAATATTTCCCAATTTATGACAAATTAACGTAACCAATAGAAAGAAAGCAACTA 918
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 919 ACAAGGAAGTATATACAGATCCAGTGGG 947

RESULT 12
US-11-108-389-87
; Sequence 87, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn


```
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnail
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ PRIOR FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ NUMBER OF SEQ ID NOS: 134
/ TYPE: DNA
/ LENGTH: 2019
/ ORGANISM: Bacillus thuringiensis (mutated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(2019)
US-11-108-389-87
```

```
Query Match      4.7%; Score 101.8; DB 7; Length 2019;
Best Local Similarity 58.6%; Pred. No. 8,6e-15;
Matches 228; Conservative 0; Mismatches 137; Indels 24; Gaps 2;
```

```
QY 661 AAAGCTGAATATATATATATGCTAGTATGTCAGACCTGCAATGATGATTTATTAATA 720
DB 583 AATTTGAAATACCATTTCTTACTGATATGCAATGAGCACCACCTTCAATTAAGTTTA 642
QY 721 TTAAGGAGCGCGTCAATTAATTAATAAAGAAATGGGGAATAGTGTGCCACCGTTGATCCA 780
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 781 GGGTCAGGAGAACTGATTTGTAACGACCGGTAAAGCCAAATTAAGATTAATTAAT 840
DB 685 ACAACTACTATTAATTAATTAATTAATGATCGTCAATATGAACTCTGAGAAATTTCTGAT 744
QY 841 TATTTGTAGGCTGATTAACAAGGGTTTATGATCAAGTAAAGAGCGGTATGATGCT 900
DB 745 CACTGTGTAAGTGTATGAACTGGTTTGAACAATTTAA-----GGCAGAGCGCT 798
QY 901 GAAGTTTGTGCAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATGATTAAT 960
DB 799 AAACAATGGGTGATCAATTAACAATTCGTAAGAAATGACACTGGCGGTTTAAATGTT 858
QY 961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTGAAGTTA 1020
DB 859 GTTGCAATTAATCCCAATTTATGACACAAATACGTAACCCAAATAGAAAGCAACAATA 918
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 919 ACAAGGAAATTAATACAGATCCAGTGGG 947
```

```
RESULT 13
US-11-058-727-59
/ Sequence 59, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnail
/ APPLICANT: James F.H. Wong
```

```
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ FILE REFERENCE: 35718/287809
/ CURRENT APPLICATION NUMBER: US/11/058,727
/ PRIOR FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2003-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 59
/ LENGTH: 2019
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis (mutated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(2019)
US-11-058-727-59
```

```
Query Match      4.7%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 2.1e-14;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;
```

```
QY 661 AAAGCTGAATATTTATTTGCTACGATATGTCAGACCTGCAATGATGATTTATTAATA 720
DB 583 AATTTGAAATACCATTTCTTACTGATATGCAATGAGCACCACCTTCAATTAAGTTTA 642
QY 721 TTAAGGAGCGCGTCAATTAATTAATAAAGAAATGGGGAATAGTGTGCCACCGTTGATCCA 780
DB 643 TTAAGGAGCGCGTCAATTTTGGAGAAATGGGGA-----TGGTCA 684
QY 781 GGGTCAGGAGAACTGATTTGTAACGACCGGTAAAGCCAAATTAAGATTAATTAAT 840
DB 685 ACAACTACTATTAATTAATTAATTAATGATCGTCAATATGAACTCTGAGAAATTTCTGAT 744
QY 841 TATTTGTAGGCTGATTAACAAGGGTTTATGATCAATGACAGCGGTATGATGCT 900
DB 745 CACTGTGTAAGTGTATGAACTGGTTTGAACAATTTAA-----GGCAGAGCGCT 798
QY 901 GAAGTTTGTGCAATTTAATAATTTCTGAGAAATGACGTTGGCGGTATGATTAAT 960
DB 799 AAACAATGGGTGATCAATTAACAATTCGTAAGAAATGACACTGGCGGTTTAAATGTT 858
QY 961 ATTGCTATATTTCCAACTTATGATTTGAAAAATATCCATTAGCAACAAGTGAAGTTA 1020
DB 859 GTTGCAATTAATCCCAATTTATGACACAAATACGTAACCCAAATAGAAAGCAACAATA 918
QY 1021 ACTAGGAAATTTATACAGATCCAGTGGG 1049
DB 919 ACAAGGAAATTAATACAGATCCAGTGGG 947
```

```
RESULT 14
US-11-058-727-91
/ Sequence 91, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnail
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ FILE REFERENCE: 35718/287809
```

```
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-91
```

```
Query Match          4.7%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 2.1e-14;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;
```

```
QY 661 AAAGCTGAATATATTATATGCTACGATGTGCAAGCTGCAATGTGCAATTTTACTA 720
   |||||
DB 583 AATTTGAAGTACCACTTCTTACTGATATATGCAATGCGCAACCTTCAATTTACTGTTA 642
   |||||
QY 721 TTAAGGACGCGAGTTAAATATTAATAAAGAAATGGGACTAGTGTGTCCACCGTTGATCCA 780
   |||||
DB 643 TTAAGGACGCGAGTTAAATATTAATAAAGAAATGGGACTAGTGTGTGTCTCA 684
   |||||
QY 781 GGGTCAGGAGAACTGATTTGTACGAGCGGTTAAAGCGAAATTAAGATATATCTAAT 840
   |||||
DB 685 ACAACTACTATTAATACTATTATGATCGTCAATGAACTTACTGCAATATTTCTGAT 744
   |||||
QY 841 TATTTGTAGGCGGTGATTAACAAGGTTTATGATGATTAAGACAGGCGGTTACAGTCT 900
   |||||
DB 745 CACTGTGTAAGTGTATGAACTGTTTGTAGCAAAATTAATAA-----GGCAGAGCGCT 798
   |||||
QY 901 GAAGTTTGTGCGAAATTAATTAATTTGCTAGAGAAATGACGTTGGCGGTATTTGATATT 960
   |||||
DB 799 AAACAATGGGTGCTGCTATTAACCAATTCGTRAGAAATGACATGCGGTTTATGATGTT 858
   |||||
QY 961 ATTGCTATATTTTCAACTTATGATTTTGAATAATATCCATTAGCAACAAGTATAGTTA 1020
   |||||
DB 859 GTTGCAATTTATCCCAATTTATGACACAAATACGTAACCAATGGAACGAAAGCAACTA 918
   |||||
QY 1021 ACTAGGGAATTTTATACAGATCCAGTGGG 1049
   |||||
DB 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947
   |||||
```

RESULT 15

```
US-11-108-389-59
; Sequence 59, Application US/11/108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prensail
; APPLICANT: James F.H. Wong
; APPLICANT: Gao-Guo Yu
; TITLE OR INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
```

```
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-108-389-59
```

```
Query Match          4.7%; Score 100.2; DB 7; Length 2019;
Best Local Similarity 58.4%; Pred. No. 2.1e-14;
Matches 227; Conservative 0; Mismatches 138; Indels 24; Gaps 2;
```

```
QY 661 AAAGCTGAATATATTATATGCTACGATGTGCAAGCTGCAATGTGCAATTTTACTA 720
   |||||
DB 583 AATTTGAAGTACCACTTCTTACTGATATATGCAATGCGCAACCTTCAATTTACTGTTA 642
   |||||
QY 721 TTAAGGACGCGAGTTAAATATTAATAAAGAAATGGGACTAGTGTGTCCACCGTTGATCCA 780
   |||||
DB 643 TTAAGGACGCGAGTTAAATATTAATAAAGAAATGGGACTAGTGTGTGTCTCA 684
   |||||
QY 781 GGGTCAGGAGAACTGATTTGTACGAGCGGTTAAAGCGAAATTAAGATATATCTAAT 840
   |||||
DB 685 ACAACTACTATTAATACTATTATGATCGTCAATGAACTTACTGCAATATTTCTGAT 744
   |||||
QY 841 TATTTGTAGGCGGTGATTAACAAGGTTTATGATGATTAAGACAGGCGGTTACAGTCT 900
   |||||
DB 745 CACTGTGTAAGTGTATGAACTGTTTGTAGCAAAATTAATAA-----GGCAGAGCGCT 798
   |||||
QY 901 GAAGTTTGTGCGAAATTAATTAATTTGCTAGAGAAATGACGTTGGCGGTATTTGATATT 960
   |||||
DB 799 AAACAATGGGTGCTGCTATTAACCAATTCGTRAGAAATGACATGCGGTTTATGATGTT 858
   |||||
QY 961 ATTGCTATATTTTCAACTTATGATTTTGAATAATATCCATTAGCAACAAGTATAGTTA 1020
   |||||
DB 859 GTTGCAATTTATCCCAATTTATGACACAAATACGTAACCAATGGAACGAAAGCAACTA 918
   |||||
QY 1021 ACTAGGGAATTTTATACAGATCCAGTGGG 1049
   |||||
DB 919 ACAAGGGAAGTATATACAGATCCAGTGGG 947
   |||||
```

Search completed: December 19, 2005, 13:47:51
Job time : 205.901 secs

Handwritten text, possibly a signature or date, oriented diagonally.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 02:23:18 ; Search time 861.297 Seconds

(without alignments)
16597.955 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataataatgctt.....atagttattatccaatcaa 2145Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2145	100.0	2145	13	ADR89413
2	2019	94.1	2019	13	ADR89414
3	2010	93.7	2010	13	ADR89416
4	855	39.9	5980	13	ADR89400
5	747.2	34.8	2082	13	ADR89401
6	739.8	34.5	2073	13	ADR89403
7	174	8.1	1983	3	AAZ93234
8	174	8.1	3837	3	AAZ93235
9	172.4	8.0	3471	2	AAV16515
10	172.4	8.0	3471	2	AAV16515 DNA encod
11	162.8	7.6	2407	4	AAZ02478
12	133.6	6.2	4391	14	AAE61394
13	119.8	5.6	1959	4	AAZ02466
14	118.4	5.5	1986	13	ADR89411
15	118.4	5.5	2016	13	ADR89409
16	118.4	5.5	2049	13	ADR89407
17	118.2	5.5	3687	12	ADR89478
18	118.2	5.5	3932	2	AAQ64112
19	118.2	5.5	3932	2	AAZ09160

20	118.2	5.5	3934	2	AAZ95051
21	118.2	5.5	3934	2	AAZ6434
22	118.2	5.5	3934	2	AAV83927
23	117.6	5.5	1806	13	ADR89392
24	117.6	5.5	1890	13	ADR89390
25	117.6	5.5	2190	13	ADR89389
26	116.8	5.4	3684	2	AAV15222
27	116.8	5.4	3684	4	AAZ9221
28	116.8	5.4	3684	4	AAZ02489
29	113.4	5.3	2019	8	ABV93759
30	112.4	5.2	3687	4	AAZ8240
31	112.4	5.2	4173	4	AAZ02482
32	111.8	5.2	1897	2	AAV3118
33	111.8	5.2	1897	3	AAZ3905
34	111.8	5.2	1897	4	AAZ6983
35	111.8	5.2	2019	8	ABV93756
36	111.8	5.2	2019	8	ABV93757
37	111.8	5.2	3471	2	AAV16516
38	111.8	5.2	3471	2	AAZ83877
39	111.8	5.2	3471	4	AAZ02477
40	111.8	5.2	3474	4	AAH19323
41	111.8	5.2	4344	2	AAQ6782
42	111.8	5.2	4344	2	AAV9986
43	110.2	5.1	2019	8	ABV93758
44	107.8	5.0	2160	4	AAZ04855
45	107.8	5.0	2965	2	AAQ06636

ALIGNMENTS

RESULT 1
ID ADR89413 standard; cDNA; 2145 BP.
XX
AC ADR89413;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 full length coding sequence.
XX
KW 86; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
XX
XX
OS Bacillus thuringiensis.
XX
FH
FT Key
FT CDS
FT
FT
FT
XX W02004074462-A2.
XX
XX
XX 02-SEP-2004.
PF 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX

PA (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89415.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 25; 178bp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
XX Sequence 2145 BP; 710 A; 338 C; 441 G; 656 T; 0 U; 0 Other:
SQ
Query Match 100.0%; Score 2145; DB 13; Length 2145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTACCACAAATATATATGTTTTTTTGTAGAAACATGTTACAGAAATATGTTGGGTACTA 60
DB 1 TTTTACCACAAATATATATGTTTTTTTGTAGAAACATGTTACAGAAATATGTTGGGTACTA 60
QY 61 CGAATATATAGAAAGACCTGGCATATATTTATTTAGTGTCTTAAAAAATAGGACTATA 120
DB 61 CGAATATATAGAAAGACCTGGCATATATTTATTTAGTGTCTTAAAAAATAGGACTATA 120
QY 121 TAAAGAGTAAATATGAAATCTTATCAAAATCAAAATGAAATGAAATTCGATGGT 180
DB 121 TAAAGAGTAAATATGAAATCTTATCAAAATCAAAATGAAATGAAATTCGATGGT 180
QY 181 TCCCGCAATACACAAATATGTCAAACAGATATCTTTTGCAAAGGATCCAAATATATTT 240
DB 181 TCCCGCAATACACAAATATGTCAAACAGATATCTTTTGCAAAGGATCCAAATATATTT 240
QY 241 CCTATTAACCTGACGCTTGTCAGGAAGCCATGCGAAGATACGTGGAATCGATCTCG 300
DB 241 CCTATTAACCTGACGCTTGTCAGGAAGCCATGCGAAGATACGTGGAATACGTCTCG 300
QY 301 GATATAGTACTATTTGGGACATACCTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
DB 301 GATATAGTACTATTTGGGACATACCTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
QY 361 ATTCTGTATATTTTCAATATTAACAAACGATTCGCTTCTGTGCAATCTGTGGCA 420
DB 361 ATTCTGTATATTTTCAATATTAACAAACGATTCGCTTCTGTGCAATCTGTGGCA 420
QY 421 GCACCTTTCTATGTGATTTAGTATCTATAATTCGTAAGAGGTAGACGAGCGGTGA 480
DB 421 GCACCTTTCTATGTGATTTAGTATCTATAATTCGTAAGAGGTAGACGAGCGGTGA 480
QY 481 AGTGAAGGGGTGACAGATTTTGAAGGTGAATGCTCTATCAAGATTTATCTTCAT 540
DB 481 AGTGAAGGGGTGACAGATTTTGAAGGTGAATGCTCTATCAAGATTTATCTTCAT 540
QY 541 TATCTTGAGGATTTGCTTACAGATTAATCTTAATAAACTTGTGTCAGTATTA 600
DB 541 TATCTTGAGGATTTGCTTACAGATTAATCTTAATAAACTTGTGTCAGTATTA 600

QY 601 CAGTTCGAAGCAGCGGGAAGAGATTTCTAACTTTAGCAGGGCTATATCAAGACAG 660
DB 601 CAGTTCGAAGCAGCGGGAAGAGATTTCTAACTTTAGCAGGGCTATATCAAGACAG 660
QY 661 AAAGCTGAATATTTATTTGCTACGTATGTCAGAGTGCMAATGTCAATTTATTA 720
DB 661 AAAGCTGAATATTTATTTGCTACGTATGTCAGAGTGCMAATGTCAATTTATTA 720
QY 721 TTAAGGACGCGATTTAAATTAATAAAGATGAGGACATAGTGTGCCACCGTTATCCA 780
DB 721 TTAAGGACGCGCGATTTAAATTAATAAAGATGAGGACATAGTGTGCCACCGTTATCCA 780
QY 781 GGGTACAGGAGAACGATTTGTACAGAGGGTTAAAGGAAATTAAGATATCTAT 840
DB 781 GGGTACAGGAGAACGATTTGTACAGAGGGTTAAAGGAAATTAAGATATCTAT 840
QY 841 TATTTGTAGGGGTGTATTAACAAGGTTTATGATCAAGATTAACAAGCGGGTCAAGTGT 900
DB 841 TATTTGTAGGGGTGTATTAACAAGGTTTATGATCAAGATTAACAAGCGGGTCAAGTGT 900
QY 901 GAACTTTGGTCCAAATTTATTAATTTGTAGAGAAATGACGTTGGCGGTATGATAT 960
DB 901 GAACTTTGGTCCAAATTTATTAATTTGTAGAGAAATGACGTTGGCGGTATGATAT 960
QY 961 ATTTGCTATTTTCCAACTTATGATTTTGAATAATTCATTTAGCAACAAGTATAGTTA 1020
DB 961 ATTTGCTATTTTCCAACTTATGATTTTGAATAATTCATTTAGCAACAAGTATAGTTA 1020
QY 1021 ACTAGGAAATTTATATACAGATTCAGTGGGATATTCAGGGGGAAATTTATGTTGGAA 1080
DB 1021 ACTAGGAAATTTATATACAGATTCAGTGGGATATTCAGGGGGAAATTTATGTTGGAA 1080
QY 1081 TTTTGTAGCTTTAATTCGTTAGACGAAATGGAACAAGGGAATGATTTTACTTGG 1140
DB 1081 TTTTGTAGCTTTAATTCGTTAGACGAAATGGAACAAGGGAATGATTTTACTTGG 1140
QY 1141 CTTCAAGCTATGATATATATGATTCATTTATATCTTACCTGGTATCTTATGTTGG 1200
DB 1141 CTTCAAGCTATGATATATATGATTCATTTATATCTTACCTGGTATCTTATGTTGG 1200
QY 1201 TGGGGGGGAACTCGTCAATATGAAAGCTTCAAAAGGGTAAACGTCCTTTCAACGAT 1260
DB 1201 TGGGGGGGAACTCGTCAATATGAAAGCTTCAAAAGGGTAAACGTCCTTTCAACGAT 1260
QY 1261 TCTGGAACCTACGATATATATCAGATATATTTTGGCAATACCGATATATTTAA 1320
DB 1261 TCTGGAACCTACGATATATATCAGATATATTTTGGCAATACCGATATATTTAA 1320
QY 1321 ATTTATTTCAATGCTAGATATGCAATGCAACCGTTTGGGTATTCATCCAGGGCAT 1380
DB 1321 ATTTATTTCAATGCTAGATATGCAATGCAACCGTTTGGGTATTCATCCAGGGCAT 1380
QY 1381 CTGTGTTTCACTGCGAAGATTTTTCGACAAACATTAATCTTCTGTATAGGTAAAC 1440
DB 1381 CTGTGTTTCACTGCGAAGATTTTTCGACAAACATTAATCTTCTGTATAGGTAAAC 1440
QY 1441 AGTTCTGGTACTCACAGCAATTAATCTGTGTTACAGATTTATTAAGATCTACCA 1500
DB 1441 AGTTCTGGTACTCACAGCAATTAATCTGTGTTACAGATTTATTAAGATCTACCA 1500
QY 1501 CCTAGTCGTACAAATTAATCTCATAGATTAATAATGCGGCAATGTTCAAAATGA 1560
DB 1501 CCTAGTCGTACAAATTAATCTCATAGATTAATAATGCGGCAATGTTCAAAATGA 1560
QY 1561 TCCAGAGTTAAGCTATTTGGTTGACACATCAAGATATGAATAAAGATATGCAATTTAT 1620
DB 1561 TCCAGAGTTAAGCTATTTGGTTGACACATCAAGATATGAATAAAGATATGCAATTTAT 1620
QY 1621 CCAGATTAATTTACGCAATTTCTGCAAGTAAAGCTTTTCCCTACAGACGATACAGGA 1680
DB 1621 CCAGATTAATTTACGCAATTTCTGCAAGTAAAGCTTTTCCCTACAGACGATACAGGA 1680

QY	1681	TATCAGAGAGTTTACGTACAGCTCGGCGCTGGTATACAGAGAGAGATGTGTACCTTA	1740
Dp	1681	TATCAGAGAGAGTTACGTACAGCTCGGCGCTGGTATACAGAGAGAGATGTGTACCTTA	1740
QY	1741	CCTTATCAGCAAGTTTAAAAATAAGTTTAACTTCTGCAACCACCAATTAATAATTCAGT	1800
Dp	1741	CCTTATCAGCAAGTTTAAAAATAAGTTTAACTTCTGCAACCACCAATTAATAATTCAGT	1800
QY	1801	GTTAGACTTCGCTACGGAGGAGGAGACCTGCTCGCTCCGAGTACGAAAGATGTGTCCCA	1860
Dp	1801	GTTAGACTTCGCTACGGAGGAGGAGACCTGCTCGCTCCGAGTACGAAAGATGTGTCCCA	1860
QY	1861	AGTTCGTGTTCAAAATGCTAATTTTTTCTCGTCAGCTACAGGTGCTATAGTTCATTGGAT	1920
Dp	1861	AGTTCGTGTTCAAAATGCTAATTTTTTCTCGTCAGCTACAGGTGCTATAGTTCATTGGAT	1920
QY	1921	TATGTGCAACACCTTAGTTACTACATTTTATCAATCAGGTGTTGAATATATTATACCAAT	1980
Dp	1921	TATGTGCAACACCTTAGTTACTACATTTTATCAATCAGGTGTTGAATATATTATACCAAT	1980
QY	1981	CTATCTGGTTTACCAACCTTATGTGGACAAATGCAATTTATCCCAATTTGACATCCAAAT	2040
Dp	1981	CTATCTGGTTTACCAACCTTATGTGGACAAATGCAATTTATCCCAATTTGACATCCAAAT	2040
QY	2041	GAAAAATGTACGAATAATGTCAAATTCGAAGAGACATATGTAGATGTGAAGAGTACCAATCC	2100
Dp	2041	GAAAAATGTACGAATAATGTCAAATTCGAAGAGACATATGTAGATGTGAAGAGTACCAATCC	2100
QY	2101	TTGGAAACAAAAAAGAGATGTGTAATGTGTTATTTATCAATTTAA	2145
Dp	2101	TTGGAAACAAAAAAGAGATGTGTAATGTGTTATTTATCAATTTAA	2145

RESULT 2	
ADNR89414	
ID	ADNR89414 standard; cDNA; 2019 BP.
XX	
AC	
ADNR89414;	
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	AXMI-008 coding sequence.
XX	
KM	ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KM	expression cassette; transformation; transgenic; plant; bacteria;
KM	lepidoptera; coleoptera; pest; pesticide; resistance;
XX	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
XX	
FH	Key
FT	Location/Qualifiers
CD	1..2019
FT	/*tag= a
FT	/product= "AXMI-008"
FT	/transl_except= pos:1..3, aa:Met
XX	
PN	MO2004074462-A2.
XX	
PD	02-SEP-2004.
XX	
PF	20-FEB-2004; 2004MO-US005829.
XX	
XX	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.
PR	20-FEB-2003; 2003US-0448797P.
PR	20-FEB-2003; 2003US-0448806P.
PR	20-FEB-2003; 2003US-0448810P.
PR	20-FEB-2003; 2003US-0448812P.
PR	19-FEB-2004; 2004US-0078197P.
PR	19-FEB-2004; 2004US-0078202P.
PR	19-FEB-2004; 2004US-0078209P.
PR	19-FEB-2004; 2004US-0078214P.
PR	19-FEB-2004; 2004US-0078257P.

PR	19-FEB-2004; 2004US-00783417.
XX	(ATHE-) ATHENIX CORP.
PA	
XX	
P1	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX	
XX	WPI; 2004-635574/61.
DR	P-PSDB; ADR89415.
PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT	and polypeptides, useful for killing lepidopteran or coleopterian pests or
PT	for producing organisms with pesticide resistance.
XX	
PS	Claim 1; SEQ ID NO 26; 178bp; English.
XX	
CC	This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC	endotoxin coding sequences of the invention have alternative start
CC	codons, producing more than one protein from a single open reading frame.
CC	The nucleic acid sequences of the invention are useful in DNA constructs
CC	or expression cassettes for transformation and expression in plants and
CC	bacteria. The nucleic acids and corresponding polypeptides are useful for
CC	killing lepidopteran or coleopterian pests. Compositions containing the
CC	delta-endotoxins of the invention, and methods for their production, are
CC	useful for the production of organisms with pesticide resistance,
CC	specifically bacteria and plants. These organisms are useful for
CC	generating altered or improved delta-endotoxin or delta-endotoxin-
CC	associated proteins that have pesticidal activity, or for detecting the
CC	presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC	nucleic acids in products or organisms.
SQ	
XQ	Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;
	Query Match 94.1%; Score 2019; DB 13; Length 2019;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	127 GTGAAAATATGAATTCTTATCAAAATACAAATGATATGAAATTCGGATGTTCGCCG 186
Db	1 GTGAAAAATVATGAATCTTATCAAAAATAACAATGAATGAATTCGATGTTCGCCG 60
QY	187 AATAAGCAAATATGTCAMACAGATATCCTTTTGSCAAGAAGATCCAATATATTTCCATT 246
Db	61 AATAAGCAANATATGTCAACAGATATTCCTTTGCAGAGATCCAAATATATTTCTATT 120
QY	247 AACCTGACGCTTGTCCAGGAGGCGCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 306
Db	121 AACCTGACGCTTGTCCAGGAGGCGCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 180
QY	307 GTAACATATGGGACATACCTTATACATTTCTGTAGAACCCGGTATATAGGTGAATTCCT 366
Db	181 GTAACATATVGGGACATACCTTATACAAATTCCTGTAGAACCCGGTATATAGGTGAATTCCT 240
QY	367 GTAATATTTTCAATTAATTAACAACAACTATCCGCTCTGGTCAATCTGAGGACGACTT 426
Db	241 GTAATATTTTCAATTAATTAACAACAACTATTCGGCTTCTGTCAATCTGAGGACGACTT 300
QY	427 TCATATATGATATTTAGTATCTATATATTCGTAAGAGGTAGACGAGACCGTGTAAAGTGAC 486
Db	301 TCATATATGATATTTAGTATCTATATATTCGTAAGAGGTAGACGAGACCGTGTAAAGTGAC 360
QY	487 GGGGTTCAGATTTTGGAGGTGAATGACGTGCTATCAAGATTATATCTTCAATATCTT 546
Db	361 GGGGTTCAGATTTTGGAGGTGAATGACGTGCTATCAAGATTATATCTTCAATATCTT 420
QY	547 GAGGATTTGGCTTACAGATTAATCAAAATCCTTAACAACTTGTGTCAGTAGTTAAACAGTTC 606
Db	421 GAGGATTTGGCTTACAGATTAATCAAAATCCTTAACAACTTGTGTCAGTAGTTAAACAGTTC 480
QY	607 CAAGCAGAGGGAAGAGATTCACTAACTTTTGGACAGGTCATTATCAAGACGAAAGCT 666
Db	481 CAAGCAGAGGGAAGAGATTCACTAACTTTTGGACAGGTCATTATCAAGACGAAAGCT 540
QY	667 GAATATATATATATGATCCCTAAGTATGCGAAGCTGCAAAATNGCATTTATTAATTAAGG 726

```
Db 541 GAAATATTATTATGCTTAGTATGCAAGTCGCAAAATGCAATTTACTATTAAAG 600
Qy 727 GAGCGATTAAATATATAAAGAAATGGGACCTAGTGTCTCACCCTTTGATCCAGGCTCA 786
Db 601 GAGCGATTAAATATATAAAGAAATGGGACCTAGTGTCTCACCCTTTGATCCAGGCTCA 660
Qy 787 GGGAGAACTGATTTGTAACGAGCGTTTAAAGCCGAAATATAAGATTAATTAATTG 846
Db 661 GGGAGAACTGATTTGTAACGAGCGTTTAAAGCCGAAATATAAGATTAATTAATTG 720
Qy 847 GTAGGTTGATTAACAAGGTTTATAGATCAGATTAAGACAGCGGCTACAACTGCTGAAGT 906
Db 721 GTAGGTTGATTAACAAGGTTTATAGATCAGATTAAGACAGCGGCTACAACTGCTGAAGT 780
Qy 907 TGGTCCAAATTTATTAATTTCTGTAAGAAATGACGTGGCGGTATTTGATTAATTGCT 966
Db 781 TGGTCCAAATTTATTAATTTCTGTAAGAAATGACGTGGCGGTATTTGATTAATTGCT 840
Qy 967 ATATTTCCAATTTATGATTTTGAATAATATCATTTAGCAACAAGTGAAGTTAACTAGG 1026
Db 841 ATATTTCCAATTTATGATTTTGAATAATATCATTTAGCAACAAGTGAAGTTAACTAGG 900
Qy 1027 GAAATTTATACAGATTCAGTGGGATATTCAGGGGAAATTTATGTTGGGAACGGTTTTT 1086
Db 901 GAAATTTATACAGATTCAGTGGGATATTCAGGGGAAATTTATGTTGGGAACGGTTTTT 960
Qy 1087 AGCTTTAATTCGGTATAGCAAGCAATGGAACCGGGACCTTGTTAGTTACTTGCTTCAA 1146
Db 961 AGCTTTAATTCGGTATAGCAAGCAATGGAACCGGGACCTTGTTAGTTACTTGCTTCAA 1020
Qy 1147 GCTATAGATATATATAGTCAATTCATTAATCTTCAAGTTGGTATCTTAGTGGCTGGGG 1206
Db 1021 GCTATAGATATATATAGTCAATTCATTAATCTTCAAGTTGGTATCTTAGTGGCTGGGG 1080
Qy 1207 GGAATCTGCTATTATGAGAAGCTTCAAAAGGGTAAACGGTCTTTTCAACGTATGTCGA 1266
Db 1081 GGAATCTGCTATTATGAGAAGCTTCAAAAGGGTAAACGGTCTTTTCAACGTATGTCGA 1140
Qy 1267 ACTACAGATTAATACCACTTAATATTTTGGCAATCCGATATATTTAAATTAATTT 1326
Db 1141 ACTACAGATTAATACCACTTAATATTTTGGCAATCCGATATATTTAAATTAATTT 1200
Qy 1327 TCATTAGCTAGATATGCAATGCAACCGTTTGGTGGATTTCAATCCACGGCATCTGTT 1386
Db 1201 TCATTAGCTAGATATGCAATGCAACCGTTTGGTGGATTTCAATCCACGGCATCTGTT 1260
Qy 1387 TCACGTGCAGAATTTTTCCGACAACCTAAATCTTCTGTATGAGGTAAACAGTTCT 1446
Db 1261 TCACGTGCAGAATTTTTCCGACAACCTAAATCTTCTGTATGAGGTAAACAGTTCT 1320
Qy 1447 GGGTACTCAGACGAATTTGAATCTGTGTACAGGTATTAAGATCTACCACTAGT 1506
Db 1321 GGGTACTCAGACGAATTTGAATCTGTGTACAGGTATTAAGATCTACCACTAGT 1380
Qy 1507 CGTACAAATTAATCTCTAGATTAATCAATGCGGCAATGTTCAAAATGAACCTCCAGA 1566
Db 1381 CGTACAAATTAATCTCTAGATTAATCAATGCGGCAATGTTCAAAATGAACCTCCAGA 1440
Qy 1567 GTTAACTATTTGGTGGACACATACAGATATGAAAAAGATATTCGAATTTTCCAGAT 1626
Db 1441 GTTAACTATTTGGTGGACACATACAGATATGAAAAAGATATTCGAATTTTCCAGAT 1500
Qy 1627 AAAATTAACGAATTTCTCTGACAGTAAAGCTTTGCCCTACACAGAGGTACAGATATGCA 1686
Db 1501 AAAATTAACGAATTTCTCTGACAGTAAAGCTTTGCCCTACACAGAGGTACAGATATGCA 1560
Qy 1687 GAGGTTACGTCAACGCTGGGCGCTGTTATACAGAGAGATAGTAAGTTAACTTAACTTAT 1746
Db 1561 GAGGTTACGTCAACGCTGGGCGCTGTTATACAGAGAGATAGTAAGTTAACTTAT 1620
Qy 1747 CAAGCAAGTTTAAATATACGTTTAACTTGTGCACCCAAGATTAATTAACCGTGTAGA 1806
Db 1747 CAAGCAAGTTTAAATATACGTTTAACTTGTGCACCCAAGATTAATTAACCGTGTAGA 1806
```

```
Db 1621 CAAGCAAGTTTAAATATACGTTTAACTTGTGCACCCAAGATTAATTAACCGTGTAGA 1680
Qy 1807 CTTGCTACGCGAAGTGGAGACCTGTGCTCCGTTCCAGATTAAGAAATGGTCCGAAGTTCT 1866
Db 1681 CTTGCTACGCGAAGTGGAGACCTGTGCTCCGTTCCAGATTAAGAAATGGTCCGAAGTTCT 1740
Qy 1867 GTTAAATATGCTAAATTTTCTGTCAGCTACAGGTGCTATGATTTGATTAATG 1926
Db 1741 GTTAAATATGCTAAATTTTCTGTCAGCTACAGGTGCTATGATTTGATTAATG 1800
Qy 1927 GACACCTTAAGTTAGTACATTTAATCAATCAGGTGTTGAATTAATTAACAAATCTATCT 1986
Db 1801 GACACCTTAAGTTAGTACATTTAATCAATCAGGTGTTGAATTAATTAACAAATCTATCT 1860
Qy 1987 GGTAAACCTTATTTGTTGACAAAGTCAATTTATCCCAATTTGATCCAAATTTGAAAA 2046
Db 1861 GGTAAACCTTATTTGTTGACAAAGTCAATTTATCCCAATTTGATCCAAATTTGAAAA 1920
Qy 2047 TGTACGAAATGTCAATTCGAAGAGACATATGTAGATGTAAGAGTACAAATCCTTGGA 2106
Db 1921 TGTACGAAATGTCAATTCGAAGAGACATATGTAGATGTAAGAGTACAAATCCTTGGA 1980
Qy 2107 ACAAAAAAGAGATTGTAAATGTTTATTTATCAATTAA 2145
Db 1981 ACAAAAAAGAGATTGTAAATGTTTATTTATCAATTAA 2019

RESULT 3
AD89416
ID AD89416 standard; cDNA; 2010 BP.
XX
AC AD89416;
XX
AC 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative start site coding sequence.
XX
KM ss: gene: delta-endotoxin; delta-endotoxin associate polypeptide;
KM expression cassette; transformation; transgenic; plant; bacteria;
KM lepidoptera; coleoptera; pest; pesticide; resistance;
XX
XX Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FH 1..2010
FT CDS /*tag= a
FT CDS /product= "AXMI-008"
PN MO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448812P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
```


DB 1741 GCTAATTTCTCTGCTACAGGTGGCTATGTTGATTGATGTCACCTTA 1800
QY 1936 GTTACTACATTATTAATCAATAGGTGGTAAATATTAACAAATCTATGTTACAC 1995
DB 1801 GTTACTACATTATTAATCAATAGGTGGTAAATATTAACAAATCTATGTTACAC 1860
QY 1996 CTATTTGTTGACAAAGTCGAATTTATCCCAATGACATCCAAATGTAAGAAATGACGAA 2055
DB 1861 CTATTTGTTGACAAAGTCGAATTTATCCCAATGACATCCAAATGTAAGAAATGACGAA 1920
QY 2056 TGTCAATTGCAAGAGACATATGATGATGTAAGAGTACATCTTGAAACAAAAA 2115
DB 1921 TGTCAATTGCAAGAGACATATGATGATGTAAGAGTACATCTTGAAACAAAAA 1980
QY 2116 GAGATGTAATAGTATTATTAATCAATTA 2145
DB 1981 GAGATGTAATAGTATTATTAATCAATTA 2010

RESULT 4

ADR89400 standard; cDNA; 5980 BP.

AC ADR89400;

DT 18-NOV-2004 (first entry)

DE AXMT-008 full length coding sequence.

XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
XX expression cassette; transformation; transgenic; plant; bacteria;
XX lepidoptera; coleoptera; pest; pesticide; resistance;
XX pesticial activity.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers

XX CDS 168..2249

XX FT /*tag= a

XX FT /product= "AXMT-008"

XX FT /transl_except= pos:168..170, aa:Met

XX PN WO2004074462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004MO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 19-FEB-2004; 2004US-00781979.

XX PR 19-FEB-2004; 2004US-00782020.

XX PR 19-FEB-2004; 2004US-00782096.

XX PR 19-FEB-2004; 2004US-00782141.

XX PR 19-FEB-2004; 2004US-00782570.

XX PR 19-FEB-2004; 2004US-00783417.

XX PA (ATHE-) ATHENIX CORP.

XX PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;

XX DR WPI; 2004-635574/61.

XX DR P-SDB; ADR89402.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.

PS Claim 1; SEQ ID NO 12; 178bp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SQ Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;

Query Match 39.9%; Score 855; DB 13; Length 5980;

Best Local Similarity 71.4%; Pred. No. 2.3e-196;

Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

QY 8 AATATATATGTTTTTTTGTAGAAACATTTGTAACAGAAATCAATGGGTACTACGAATAT 67
DB 49 AATATATGAGTTTATTTGTAGAAACATTTGTAACAGAAATCAATGGGTACTACGAATAT 108
QY 68 ATAGAAAGACACCTGGCATATTTATTTAGGTCTTAAATTAAGACTATTAAGAG 127
DB 109 ATAGAAAGACACCTAAACATATTTATTTAGGTCTTAAATTAAGACTATTAAGAG 168
QY 128 TGAATAATATGAAATTTCTTATCAAAATATGAATATGAATATTCGATGTTCCCGA 187
DB 169 TGAATAATATGAAATTTCTTATCAAAATATGAATATGAATATTCGATGTTCCCGA 228
QY 188 ATACACAAATATGTCAAACAGATATCTTTGCAAGAGATCCAAATATATTTCTATTA 247
DB 229 ATACACAAATATGTCAAACAGATATCTTTGCAAGAGATCCAAATATATGTCATATAT 288
QY 248 ACCTGACCTTGTCTGAGGAGGAGCCATGCGAAGATACGTTGATCTCGAATATAG 307
DB 289 CTGGAATATATGTCAGGAGATCTCAATGGAATGAAATTTGGAGATACGTAACGATTA 348
QY 308 TAATATTTGAGCATCTTATCAATCTTCTGCTAGAACCCGGTATAGGTGAAATCTTG 367
DB 349 CAAGTATTTGGATTAATCTTATAGAGTTGTGATAGAACCTGATTTGGGTGAAATTAAT 408
QY 368 TAATATTTGAGCATCTTATCAATCTTCTGCTAGAACCCGGTATAGGTGAAATCTTG 427
DB 409 CACTATTTCAATTAATAGGAAACCTAATCCGACTAATGTCGTAACCTGTGACACTTT 468
QY 428 CTATATGATTTATGATCTATTAATCTGTAAGAGGTAGACGAGCGTTAAGTAGAG 487
DB 469 CTATATGATTTATGATCTATTAATCTGTAAGAGGTAGACGAGCGTTAAGTAGAG 528
QY 488 GGGTTCAGATTTTGAAGGGAATGACGCTTATCAAGATTAATCTTCAATATCTTG 547
DB 529 CGATTTCAAGATTTTGAAGGGAATGACGCTTATCAAGATTAATCTTCAATATCTTG 588
QY 548 AGGATTTGCTTACAG-----ATAATCAATCTTAAAAAATCTTGACAG 592
DB 589 GGGCTTTGCTTAAAGCGGTAACCACTTCAAAAGCAATATCTTGATATGGAACAT 648
QY 593 TAGTAAACAGTTCCAGACGAGGAAGAGATTTCACTAACTTTTGAAGGCTATAT 652
DB 649 TAGTAAACAGTTTAAACCTTCAAGAGAGATTTCAATGAATTTCTAGAGGGCTATAT 708
QY 653 CAAGACAGAAAGCTGAATATTTATTTGCTTACGATGAGTGAAGTGAATATGTCATT 712
DB 709 CAAGACAGAAAGCTCAAGATTTGTTTACCTTCTTGAACAGTGAATATGTCATT 768
QY 713 TATTACTATTAAGGAGCGAGTTAAATATTAAGAAATGGGAGCTAGTGTCCACCGT 772

```

Db      769 TATTACTTAAAGGATGACAGTTCATATTAAGACAATGGTCCATTTTGAAGTCAG 828
Qy      773 TGTATCCAGGCTCAGGGAGAA-----CTGATTGTA 802
Db      829 AGAATGTAGATCCGAATTAATATACCTTAACAGTGTGATTTTACCGGTGATTAAT 888
Qy      803 ACCGAGCGTTAAAGCGGAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTA 862
Db      889 ATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 948
Qy      863 AGGCTTAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 922
Db      949 TAGCTTAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
Qy      923 AATTGCTAGAAATGACGTTGGCGGTATGATTAATTAATTAATTAATTAATTAATTAAT 982
Db      1009 AATTGCTAGAAATGACGTTGGCGGTATGATTAATTAATTAATTAATTAATTAATTAAT 1068
Qy      983 ATTTTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1042
Db      1069 ATTTTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1128
Qy      1043 CAGTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1096
Db      1129 CAGTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1188
Qy      1097 CGGTAGAAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1156
Db      1189 GGTAGAGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1248
Qy      1157 TATTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1216
Db      1249 TATTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1299
Qy      1217 ATTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1276
Db      1300 ATTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1359
Qy      1277 ATTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1336
Db      1360 ATGAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1419
Qy      1337 GATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1396
Db      1420 ---TCATGAACCTTGTAGAGAGAGCTACCGCTAGACAGAGTATCGTTCAGAAAGCAG 1476
Qy      1397 AATTTTTCGACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1453
Db      1477 ATTTTTCGACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1536
Qy      1454 CACAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1513
Db      1537 GAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1590
Qy      1514 ATTAATCTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1573
Db      1591 GACCTCTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1650
Qy      1574 TATTTGTTGACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1633
Db      1651 TATTTGTTGACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1710
Qy      1634 CGCAATTTCTGACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1693
Db      1711 CACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1770
Qy      1694 ACCTCAAGCTGGGCTT 1710
Db      1771 ATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1787

```

RESULT 5
ADR89401

```

ID      ADR89401 standard; cDNA; 2082 BP.
XX      ADR89401;
AC      18-NOV-2004 (first entry)
XX      AXMI-008 coding sequence.
DE      ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW      expression cassette; transformation; transgenic; plant; bacteria;
KW      lepidoptera; coleoptera; pest; pesticide; resistance;
XX      Bacillus thuringiensis.
OS      Key
FH      Location/Qualifiers
FT      1..2082
FT      CD5
FT      /*tag= a
FT      /product= "AXMI-008"
FT      /transl_except= pos:1..3, aa:Met
XX      WO2004074462-A2.
XX      02-SEP-2004.
XX      20-FEB-2004; 2004MO-US005829.
XX      20-FEB-2003; 2003US-0448632P.
XX      20-FEB-2003; 2003US-0448633P.
XX      20-FEB-2003; 2003US-0448797P.
XX      20-FEB-2003; 2003US-0448806P.
XX      20-FEB-2003; 2003US-0448810P.
XX      20-FEB-2003; 2003US-0448812P.
XX      19-FEB-2004; 2004US-00781979.
XX      19-FEB-2004; 2004US-00782020.
XX      19-FEB-2004; 2004US-00782096.
XX      19-FEB-2004; 2004US-00782141.
XX      19-FEB-2004; 2004US-00782570.
XX      19-FEB-2004; 2004US-00783417.
XX      (ATHE-) ATHENIX CORP.
XX      Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX      WPI; 2004-635574/61.
XX      P-PSDB; ADR89402.
XX      New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX      and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX      for producing organisms with pesticide resistance.
XX      Claim 1; SEQ ID NO 13; 178bp; English.
XX      This sequence encodes an isolated delta-endotoxin. Some of the delta-
XX      endotoxin coding sequences of the invention have alternative start
XX      codons, producing more than one protein from a single open reading frame.
XX      The nucleic acid sequences of the invention are useful in DNA constructs
XX      or expression cassettes for transformation and expression in plants and
XX      bacteria. The nucleic acids and corresponding polypeptides are useful for
XX      killing lepidopteran or coleopteran pests. Compositions containing the
XX      delta-endotoxins of the invention, and methods for their production, are
XX      useful for the production of organisms with pesticide resistance,
XX      specifically bacteria and plants. These organisms are useful for
XX      generating altered or improved delta-endotoxin or delta-endotoxin-
XX      associated proteins that have pesticidal activity, or for detecting the
XX      presence of delta-endotoxin or delta-endotoxin-associated proteins or
XX      nucleic acids in products or organisms.
XX      Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;
XX

```

Query Match 34.8%; Score 747.2; DB 13; Length 2082;
Best Local Similarity 69.8%; Pred. No. 2e-170;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

OY	127	TTGAAAAATGAAATCTTATCAAAATTCAAATGAATATGAAATTCGGATGGTTCCCG	186
Db	1	GTGAAAAAGATGAAGTCATATCAAAATATGAAATATGAAATATGGAATCCTCATCG	60
OY	187	AATAACAAATATGTCAACAGAGATATCTTTTGCAAGAGATCCAAATATATTTCTATTT	246
Db	61	AATAACAAATATGCCCAACAGATATCTTTTGCAATATATCCGGAGATATGTCTATCTATG	120
OY	247	AACCTGACCGCTTGTCAAGGAAAGCCATGCGAAGTACGTGGAAATCAGTCTCGGATATA	306
Db	121	TCCTGGAAATGATGTGCAGGGAATCTCAATGGATGAATTTGGGAAATCAGTGCAAACGATA	180
OY	307	GTAACATATTTGGGACATACCTTATACATTTCTTGAGAAACCCGGATATGGTGAATTCCT	366
Db	181	ACAAATATTTGGGATTAATCTTATAGAGTTTGTATAGAACTTATTTGGTGGAAATTAAT	240
OY	367	GTAATATTTTCAATATATAAACAACTCATTCGCTTCTGGTCAATCTGTGGACACCTT	426
Db	241	ACACTATATCAATATATAGAAATCAATATTCGATATTCGTCAAACTGTGTCAAGACTT	300
OY	427	TCCTATATGATTTATGATCTATATATTCGTAAAGGATAGACGAGGCTGTAAAGTAC	486
Db	301	TCCTATATGATTTATGATCTATATATTCGTAAAGGATAGACGAGATGTTTAAAGTAT	360
OY	487	GGGGTTCAGATTTTTCAGGGTGAATGACGTCTTATCAAGATTTATATCTTCATATCTT	546
Db	361	GCGATTTGAGATTTTTCAGCGTAAATGAAATATTAAGAGTATATCTTTCTTATCTT	420
OY	547	GAGATTTGGCTTACG-----ATATATCAATCTTAAAAAATTGCTGAC	591
Db	421	GGGGCTTGGCTTAAAGACGTAAACCACTTCAAAAGACAAATATTTCTGATATGACAA	480
OY	592	GTAGTTAAACAGTTTCCAGACACGGGAAAGATTTCACTAACTTTTGACGGGTCACTTA	651
Db	481	TTAGTTTATATTTTAACTTTTAAAGATTTTCAATGAAATTTCTAGAGGGTCAATTG	540
OY	652	TCAGACAGAAAGCTGAAATATTTATTTGCTTACGATATGTCAGATGCAAGCTGCAATGTGCAT	711
Db	541	TCAGAAACCAATGCTCAAGTATTTGTTATTACTTATTTGCACAAGCTGCAAAATGTGACG	600
OY	712	TTATATCATTTAAAGGACGAGTTTAAATATTAATAAAGATGGGACCTGTGTGTCCACCG	771
Db	601	TTATATCATTTAAAGGATGACGTTCAATATATTAAGACAAATGTGTCCATTTTGAATGCA	660
OY	772	TTGTATCCAGGTCAGGAGAA-----CTGATGT	801
Db	661	GAGAAATGTAAGATCGGAATTAATATCACCTTAACATGTGTGTGATTTACCGGTGATTAAC	720
OY	802	AACGACCGGTTAAAGCCGAAATTAAGATATCTAAATTTATGTGTAGGGTGTATTAAC	861
Db	721	TATGACCATTTAAATATGCAAAACGACAGATTAACAAATTTATTTATTTATTTGATATCAG	780
OY	862	AAGGTTTATAGATCAATATAGACAGCGGGTCAATATGCTGAAAGTTTGTTCGAAATTTAAT	921
Db	781	GTAGGTTTAAATCAATATTAACACGGGGGGGACAGGTCTGCACATCTGTTCGAAATTTAAT	840
OY	922	AAATTTCTGTAGAAATATGACGTTGGCGGTATGTGATATTTATTTCTATATTTTCCAACTTAT	981
Db	841	AAATTTCTGTAGAAATATGACGTTGGCGGTATGTGATATTTATTTCTATATTTTCCAACTTAT	900
OY	982	GATTTTGGAAAAATATCCATTTAGCAACAGTGTAGATTAACATAGGAAATTTATATACAT	1041
Db	901	GATTTTGGAAATATATCCATTTGCAACATGTAGATTTGACATAGGGAATTTATATACAT	960
OY	1042	CCAGTGGATATTTCAAGGGGAAATTTATGTTGGGAACGTTTT-----TTAGCTTTAAT	1095
Db	961	GCAGTGGATATTTCAATCCGGAACTTATGTTGTTACGGAATTTGCGCTAATATCTTTAAT	1020
OY	1096	TCGATAGAAAGCAATATGAAACACGGGGAACCTGGTTTATGTTACTTGGCTTCAAGCTATAGAT	1155
Db	1021	GGGTTAGAGGCTTAAATGAAACACGGGGAACCTGGTTTATGTTACTTGGCTTCAAGCAATAGAT	1080

QY	1156	TTATATAGTCACTTCATTAATCACTTCACCTGCTGTATCTTACTGCTGGGGGGAACCTG	1215
Db	1081	ATATATATATATGATGATTT-----TCGAGATATTTTGGCGGCTGGGATGGAACCTG	1131
QY	1216	CATTATGAAGCTTCACAAAGGGTAAACGGTCTTTTCAACGTAATGCTGGAACCTACGAGT	1275
Db	1132	CATTATGAAGCTTCACAAAGGGTAAACGGTCTTTTCAACGTAATGCTGGAACCTACGAGT	1191
QY	1276	AATAATCCAGTAAATATATTTTGGCAATACGATATATTTAAATTAATTCATTAAGT	1335
Db	1192	AATGATCTAGTAATATTAATTAATTTTTCAGATGCCATGTAATTAATTAATTAATTAAGT	1251
QY	1336	AGATATGCAATGCAACCGTTTGGGGTATTCATCCACGGCACTTCTGTTCCAGTGCA	1395
Db	1252	A---TCATGAACCTAGTAGAGAGACTACCGCTGAGCCAGATGTCGTGTTTCAAAAGCA	1308
QY	1396	GAATTTTTTCCGACAACCTAAATACCTTCCGTATGAGGTAAACGTTCTGGG---TAC	1452
Db	1309	GATTTTGTAGGATGAGGGGACCTGATTTAAATTAATGATGCAAGTAATATAGGCTTAAGC	1368
QY	1453	TCACAGCAATTTGAATCTGTTGTACCAAGTATTAATAGATCTACCACTAGTCTGACA	1512
Db	1369	AGATATGCAATTTGAATCTAGTTCCTCACTTTG-----ATTGCACTGAATGATGTTAGA	1422
QY	1513	AATTAATCTCTAATGATTTCAAATGCGGCATGTGTCAAATGAACCTCCAGATTAAAC	1572
Db	1423	GGACCCCTCTCTAATGATTTCAAATGCGGCATGTGTCAAATGAACCTCCAGATTAAAC	1482
QY	1573	GTAATTTGGTTGGACACATACAAAGTATGAAAAAGATATGCAATTTATCCAGATTAAT	1632
Db	1483	GTAATTTGGTTGGACACATACAAAGTATTAACGTAATTAATTAATTAATTAATTAATTAAT	1542
QY	1633	ACGCAAAATTCCTGCAATTAAGCTTTTGGCCCTACAGACAGGTACAGATATGCAAGAGT	1692
Db	1543	ACACAAATACCGGGGTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1602
QY	1693	TACGTACACGCTGGGCTT 1710	
Db	1603	TATGTAATTAATAAGGCACT 1620	
RESULT 6			
ADDR89403			
ID	ADDR89403 standard; cDNA; 2073 BP.		
AC			
XX	ADDR89403;		
DT	18-NOV-2004 (first entry)		
DE	AXMI-008 alternative start site coding sequence.		
KW	ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;		
KW	expression cassette; transformation; transgenic; plant; bacteria;		
KW	lepidoptera; coleoptera; pest; pesticide; resistance;		
XX	pesticidal activity.		
OS	Bacillus thuringiensis.		
XX			
FH	Key		
FT	Location/Qualifiers		
FT	CDS		
FT	1..2073		
XX	/*tag= a		
XX	/product= "Alternative AXMI-008"		
PN	WO2004074462-A2.		
XX			
PD	02-SEP-2004.		
PF	20-FEB-2004; 2004WO-US005829.		
PR	20-FEB-2003; 2003US-0448632P.		
PR	20-FEB-2003; 2003US-0448633P.		
PR	20-FEB-2003; 2003US-0448797P.		
PR	20-FEB-2003; 2003US-0448806P.		

CC This sentence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

Query Match	34.5%;	Score 739.8;	DB 13;	Length 2073;
Best Local Similarity	69.7%;	Pred. No. 1.3e+168;		
Matches 1135; Conservative	0;	Mismatches 422;	Indels 72;	Gaps 7;

Oy	136	ATGAATTCCTAATAAAATCAAAATGAAATGAAATTCGGAAGGTTCCCGAATTAACA	195
Db	1	ATGAGTCATATCAAAATATAAAATGAAATTAAGAAATTAATGGAAATCCTCAATGAATAACA	60
Oy	196	AATATGCAACAGATATCCTTTGGAAAGATCCAAATATATTCATATTAACGTGAC	255
Db	61	AATAGCGCAACGATATTCCTTTTGGAAATATCGGATATGTCTAATATGCTTGGAAAT	120
Oy	256	GCTTGTCAAGGAAGGCCATGCGAAGATACGTGGGAATCAGTCCGATATATGTAATTT	315
Db	121	GATTGTCAAGGAATCTCATGGAGTGAATTTTGGGAATCAGTCGAACGATACAAAGTAT	180
Oy	316	GGGACATACCTTATACAAATCTTCTGTAGAACCCTGATAGTGAATTCCTGATATATT	375
Db	181	GGGATTAATCTTATAGAGTTTGTGAATAGCAACTAGTTTGGTGGAAATTAATACACTATTA	240
Oy	376	TCATATATATAAACAACCAATCCGCTTCTGTGCATCTGTGGCGACCTTTCTATATGT	435
Db	241	TCATATATAGAAAACCAATCCGACTAATCGTCAAACTGTCTGACCTTCTATATGT	300
Oy	436	GATTTAGTATCTAATATCGTAAAGAGTAGACGAGCGGTATTAAGACGGGGTTGCA	495
Db	301	GATTATATTCTAATATCGTAAAGAGTAGACCGAATAGTTTAAAGTAGATGCATTTGCA	360
Oy	496	GATTTAGGGTGAATAATGACTGCTTATCAAGATTTATCTTCATTTCTTGAGAGATTGG	555
Db	361	GATTTGACCGTAAATTTGAAAAATTTATAGAGATTTATCTTCTTATCTGGGGCTTGG	420
Oy	556	CTTACG-----ATAATCAATCCATAAAACTTGCTGACGTAGTTAAA	600

[illegible]

QY 1642 CCGAGTAAAGCTTTTGGCCCTACAGCAGATATGACAGAGGTACGTCA 1701
DB 1543 CCGCGGTGAAGAGTATTACTTCAAAATATCTGTAACTCATACCTATGTA 1602
QY 1702 GCTGGGCTT 1710
DB 1603 AAAGCACT 1611

RESULT 7
AA293234
ID AA293234 standard; DNA; 1983 BP.
XX
AC AA293234;
XX
DT 04-JUL-2000 (first entry)
XX
DE Sequence encoding truncated Cry9Aa toxin.
XX
KM Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
de.
XX
OS Synthetic.
XX Bacillus thuringiensis; ssp. galleria.
XX
FH Key Location/Qualifiers
FT CDS 17..1966
FT /tag= a
FT /product= "Cry9Aa toxin N-terminal fragment"

XX MO200011025-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 24-AUG-1999; 99WO-F100698.
XX
XX PR 24-AUG-1998; 98FI-00001809.
XX
XX PA (UNIC-) UNICROP LTD.
XX
PI Kuvshinov V, Kanerva A, Koiyu K, Pehu E;
XX
DR WPI; 2000-224660/19.
XX
DR P-PSDB; AAY83039.
XX
PT Modified synthetic DNA sequences comprise modification of the truncated
PT Cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX plants.
XX
PS Claim 2; Page 55-57; 90pp; English.
XX
XX CC Synthetic DNA sequences derived from the sequence of the truncated cry9a
CC gene of Bacillus thuringiensis ssp. galleria can be used for the
CC production of a unique insecticidal protein having the same properties as
CC the N-terminal domain of the insecticidal protein encoded by the native
CC cry9a gene of Bacillus thuringiensis ssp. galleria. The insecticidal
CC toxin works by binding to specific receptor molecules in the gut of
CC insects with consequent formation of ion channels in the epithelium. This
CC action leads to ion efflux and paralysis of the intestinal function,
CC which causes death of the insect. The synthetic DNA sequences exhibit
CC enhanced expression through improved mRNA processing, stability, and/or
CC translation providing improved tolerance against target insects. They can
CC be used in the production of transgenic plants capable of expressing the
CC N-terminal domain of the insecticidal protein encoded by the native
CC cry9a gene. They therefore have a role in pest control and crop
CC protection
XX
XX SO Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;

Query Match 8.1%; Score 174; DB 3; Length 1983;
Best Local Similarity 54.3%; Pred. No. 1.2e-31;
Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGGATATATGATCAATTTGGGACATACCTTATACATTTCTGTAGAAC 346
DB 144 GCGATGACCAAAAGAGAGATATCTATTGGGACACATAGTCTCTTATACACAGCAC 203
QY 347 CCGGTATAGTGGAAATTCCTGTATATTTT-----CAATAATAAACAACTCAATTCGT 400
DB 204 CTTCTCTTACTGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACAGAGTA 263
QY 401 CTTCTGTATATCTGTGGACACTTCTATATGTGATTTAGTATCTATATTTGTAAG 460
DB 264 GTATGACCAATCCATATCAGATTTGTCTATATGTGACTTAATCTATATATGATTTAC 323
QY 461 AGGTAGACGAGCGGTGTTAAGTGAACGGGGTTCAGATTTTGGAGGTGAATGACTGCTT 520
DB 324 GGGTATAGTACAGTGTTTTAAATGATGGGATTGCGAATTTTAAAGTCTGTACTTAT 383
QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAGGATTTGGCTTACAGATA 565
DB 384 ACAGGAATATTTAGAGGCTCTGATAGCTGGAATAGAAATCTTAATCTGCTGTGCTG 443
QY 566 AATCAATCTTAAAAAATCTGCTGACGTATGTTAAACAGTCCAGACGAGGAAGAAT 625
DB 444 AAGAACTCGTACTCGTTTGAATGCGGACTCGAATTTGATGAAATTTTAACTCCGAG 503
QY 626 TCATTAATCTTTAGACAGGCTCATTATCAAGACAGAAAGCTGAATATTTATTTGCTTA 685
DB 504 GGTCTTAAACGAATGTGCTGTTAGCTATGACGACAAATATCCAAATATTTATTTACCT 563
QY 686 CGTATGTGACAGCTGCATTAATGTGATTTTAACTTAAAGGACGCAATTAATTAATA 745
DB 564 CTTTTCGAGCGCTGATTTTCCATTTATTACTAATAGGATGCTACTAGATATAGCA 623
QY 746 AAGATGGGACTATGTTGTCCACCGTTTATCCAGGGTCAGGAGAACTGATTTGTACG 805
DB 624 CTAAATGGGGGCTAATACATGCTACACCTTTATTA-----ATTATCAAT 668
QY 806 AGCGTTTAAAGCGAAATTAAGATTAATTAATTTGATGGGTGATTAACAAG 865
DB 669 CAAACTATGATAGCTTATTAATGAACTATATGATTTATTCGTTACATTTGATTCGAG 728
QY 866 GTTATGATCAGATTAAGACAGCGGGTACAGTGTGAACTTTGTGCAATTTAATAAT 925
DB 729 GTTCAACAGACTAAGACAAAGAGGACATAGTGTACAGCTTGTTAGAAATTCATAGAT 788
QY 926 TTGTTAGAAATATGACGTGGGTATTTGATTTATTTCTATATTTTCAACTTATGATT 985
DB 789 ATCGTAGAGATGATGATTTGATTTGATATGATGATCAATTTTCAAGTCTTGATA 848
QY 986 TTGAATAATATCCATTAGCAACAGTGTAGTTAACTGAGGAATTTATACAGATCCAG 1045
DB 849 TTACTTAATTAATCCATATGAAACAGATTTTCAAGTTAGTGGGTCAATTTATACGATCCA 908
QY 1046 TGGGATATTCAGGGGGAATTTATGTTGGAA 1077
DB 909 TTGGTTTGTATCATGTAGTATGCTTAGGGA 940

RESULT 8
AA293235
ID AA293235 standard; DNA; 3837 BP.
XX
XX AC AA293235;
XX
XX DT 15-SEP-2003 (revised)
XX
XX DT 04-JUL-2000 (first entry)
XX
DE Sequence encoding native Cry9Aa toxin.
XX
XX KM Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
de.
XX OS Bacillus thuringiensis; ssp. galleria.


```

XX Key Location/Qualifiers
FH 385..2364
FT /*tag= a
FT /product= "Cry9Aa toxin"
PN W0200011025-A1.
PD 02-MAR-2000.
PF 24-AUG-1999; 99WO-FI000698.
PR 24-AUG-1998; 98FI-00001809.
PA (UNIC-) UNICROP LTD.
PI Kuвшinov V, Kanerva A, Koiyu K, Pehu E;
DR WPI: 2000-224660/19.
DR P-PSDB; AAY82988.
PT Modified synthetic DNA sequences comprise modification of the truncated
PT cry9Aa gene of Bacillus thuringiensis for improved insect control in
PT plants.
PS Claim 10; Page 57-59; 90pp; English.
XX
XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
XX gene of Bacillus thuringiensis ssp. galleria can be used for the
XX production of a unique insecticidal protein having the same properties as
XX the N-terminal domain of the insecticidal protein encoded by the native
XX cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
XX toxin works by binding to specific receptor molecules in the gut of
XX insects with consequent formation of ion channels in the epithelium. This
XX action leads to ion efflux and paralysis of the intestinal function,
XX which causes death of the insect. The synthetic DNA sequences exhibit
XX enhanced expression through improved mRNA processing, stability, and/or
XX translation providing improved tolerance against target insects. They can
XX be used in the production of transgenic plants capable of expressing the
XX C-terminal domain of the insecticidal protein encoded by the native
XX cry9Aa gene. They therefore have a role in pest control and crop
XX protection. (Updated on 15-SEP-2003 to standardise OS field)
SQ
SQ Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;
Query Match 8.1%; Score 174; DB 3; Length 3837;
Best Local Similarity 54.3%; Pred. No. 1,4e-31;
Matches 441; Conservative 0; Mismatches 335; Indels 36; Gaps 3;
QY 287 GGGAAATCAGTCTCGATATATGTAATCTATGGACATACCTTATCAATCTTGTGTGAAC 346
DB 542 GCGATGACGAGAAAGAGACAGATCTATTTGGACACACATAGTCTCTTATCAGACAC 601
QY 347 CCGGTATAGGTGGAATTCCTGTAATTTT-----CAATATATAAAGAACTACTTCGCT 400
DB 602 CTCTCTTACTGATTAATTAATTAATAGTATAGACCTTATAGTAAGTAAGTCTAGAGATA 661
QY 401 CTCTGTGCAATCTGTGAGACACTTCTATATGTATAGTATATAGTATATATGCTGAAG 460
DB 662 GTAGTGAACAATCATATCAGATTTGTCTATATATGCTTATATCTATATATGATTTAC 721
QY 461 AGGTAGACGAGAGCGTGTATAGTACGCGGTGTGCAATTTTGAAGGTGAATGACGCTT 520
DB 722 GGGTAAAGTCAGAGGTTTAAATGATGGATGAGATTTTAATGCTTCTGTAATCTTAT 781
QY 521 ATCAAGATTAATTAATCTTC-----ATTATCTGAGAGATTTGGCTTACAGATA 565
DB 782 ACGAGAACTATTTAGAGGCTCTGATAGCTGGAATTAAGAAATCTTAATTTGCTTGTGCTG 841
QY 566 AATCAAAATCTTAAAGAACTGTGCTGACCTAGTTAAACAGTTCCAAAGCAGCGGAAGAGATT 625
DB 842 AAGAACTCCGTACTCGTTTGAATGCCGACCTCAAGATTTGATGAATTTTAAACCGGAG 901

```

```

QY 626 TCACTAACTTTTACGAGGCTCATTTACAGACAGAAAGCTGAATATTTATTTGCTTA 685
DB 902 GGTCTTTAAAGAAATGAGGCTCGTTAGCTAGACAAATATTTATTTATTTACCTT 961
QY 686 CGTATGCAAGGCTGCAATATGATATTATTTACATTAAGGAGCGGATTAATATAA 745
DB 962 CTTTGGAGCGGCTGCAATTTTTCATTTATTTACTACTAAGGAGTCTACTAGATATGCA 1021
QY 746 AAGAAATGGGACTAGTGTGTCCACCGTTGTATCCAGGCTCAGGAGAACTGATTTGTAAC 805
DB 1022 CTATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 1066
QY 806 AGCGTTAAAGCGAAATTAAGATTAATTAATTTGTTAGGCTGTGATTAACAG 865
DB 1067 CAAACTAGTAGAGCTTATGAACTATATCTAGATTAATTCGTACATTTGATTAATGAG 1126
QY 866 GTTTAGATCAGATTAAGCAGCGGCTGACAGTCTGAAAGTTTGTGCAATTTAATTAAT 925
DB 1127 GTTTCACGAACTTACAGCAAGAGGCACTAGTCTACAGCTGTGTAAGAAATTTCAATGAT 1186
QY 926 TTGTAAGAGAAATGACGTTGCGGTATTTGATATTTATTTGCTATATTTCCAACTATGATT 985
DB 1187 ATGCTAGAGAGATGACATTTATGATTTAGATTAATAGATCATTTTCAAGTCTTATA 1246
QY 986 TTGAAATATTCATTAAGCAACAGTGTAGAGTTAAGTAACTAGGAAATTTATACAGATCCAG 1045
DB 1247 TTACTAATTAATCCCAATTAAGAAACAGATTTTCAAGTTGAGTAGGCTATTTATACAGATCCAA 1306
QY 1046 TGGGATTTTACAGGCGGAAATTAATGCTTGGGAA 1077
DB 1307 TTGCTTTTGTACATCGTATGATGCTTTAGGGGA 1338
RESULT 9
AAV16515
ID AAV16515 standard; DNA; 3471 BP.
XX
XX AAV16515;
AC
XX
XX 11-JUN-1998 (first entry)
DT
XX
XX DNA encoding a Bacillus thuringiensis toxin designated 86Bb1 (a).
DE
XX
XX Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
KM Heliothis virescens; Helicoverpa zea; ss.
XX
XX Bacillus thuringiensis.
OS
XX
XX Key Location/Qualifiers
FH 1..3471
FT /*tag= a
FT CDS
XX
XX W09800546-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 01-JUL-1997; 97WO-US011658.
PF
XX
XX 01-JUL-1996; 96US-00674002.
PR
XX
XX (MYCO) MYCOGEN CORP.
PA
XX
XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhofe BA;
PI WPI: 1998-086971/08.
DR P-PSDB; AAY46856.
XX
XX New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
XX encoding toxins which are active against lepidopteran pests such as the
XX Black cutworm.
PS Example 5; Page 86-88; 183pp; English.
XX

```


CC The present sequence is isolated from a *Bacillus thuringiensis* isolate
 CC (PS86B1). It encodes a toxin designated 86B1 (a) which is active against
 CC lepidopteran pests. The toxin isolates can be used for the control of
 CC lepidopteran pests such as *Agrotis ipsilon* (black cutworm), *Heliothis*
 CC *virescens* and *Helioverpa zea*. PCR primers and probes can be derived from
 CC the polynucleotide encoding the toxin and used for the amplification and
 CC detection of other toxin-encoding sequences
 XX

SO Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;

Query Match 8.0%; Score 172.4; DB 2; Length 3471;

Best Local Similarity 54.2%; Pred. No. 3,4e-31;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

```

QY 287 GGGAAATCACTCTCGGATATAGTAACTATTGGGACATACCTTAATACATTTCTGCTAGAC 346
DB 158 GCGATGACGAAAAAGAGAGATCTATTGGGCAACACATAGTCTCTTATCACAGCAC 217
QY 347 CCGGATAGGTGGAATTCCTGTATATTTT-----CAATATATTAACAACATCATTCCGT 400
DB 218 CTTCTCTTACTGATTAATTTCAATAGTATATAGCCTTAATAGGTAAGTACTAGAGGTA 277
QY 401 CTTCTGCTCAATCTGTGGACGACCTTCTATATGTGATTTAGTATCTATATTCGTAAG 460
DB 278 GTAGTGACAAATCATAATCAGATTGTCTATATGTGACTTATATCTATATGATTTAC 337
QY 461 AGGTAGACGAGAGGTGTTAGTACGCGGCTGACATTTTGGAGGTAAGTACATGCTT 520
DB 338 GGGTAAGTCAAGATGTTTAAATGATGAGATGAGATTTTAAATGTTCTGTACTCTTAT 397
QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATGGCTTACAGATA 565
DB 398 ACAGGAATCTATTAGAGGCTCTGGATAGCTGAGATTAAGATCTTAATTCGCTTCTGCTG 457
QY 566 AATCAAAATCTTAAAAAATTGCTGACGTAGTAAACGTTCCAGACGCGGAAGAAGATT 625
DB 458 AAGAACTCCGCTACTCGTTTAAATGCGCCGACTCAGAAATTTGATAGATTTTAAACCGAG 517
QY 626 TCACATAACTTTAGCAGGCTCTTATACAGACAGAAAGCTGAATTTTATTTTGGCTTA 685
DB 518 GGTCTTTTACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCCAAATTTATTTACCTT 577
QY 686 CGTATGTCAAGCTGCAATATGTCATTTATTACTATTTAAGGACGCGATTAATATTA 745
DB 578 CTTTGGAGCGCTGATTTTTCATTTATTACTACTAAGAGATGCTACTAGATATGGCA 637
QY 746 AAGAAATGGGACTAGTGTGTCCACCGTTGATCCAGGCTCAGGAGAACTGATTTAGC 805
DB 638 CTAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
QY 806 AGCGGTTAAAGGAAAAATTAAGATATCTAATTTTGTATAGGTTGATTAACAAG 865
DB 683 CAAAATAGTAGAGCTTATTGAACTATATACGATTAATTCGTAATGGTATTAATCGAG 742
QY 866 GTTATAGTCAGATTAAGACAGCGCGGTACAGTGTCAAGTTGGTCAAAATTTAATAAT 925
DB 743 GTTTCACGAACTAAGACAGACGACCTAGTGTCAAGCTTGGTATGAAATTTCAATGAT 802
QY 926 TTGCTAGAGAAATGACGTTGCGGTATTTGATATTAATTTGCTAATTTTCAACTATGAT 985
DB 803 ATGTGTAGAGATGACATTTGATGTATTAATATATAGATCATTTTCAAGCTTGATA 862
QY 986 TTGAAAAATATTCATTAAGCAACAGTGTATAGTTAACTAGGAAATTTATACGATCCAG 1045
DB 863 TTAATAATTAACCAATAGAAACAGATTTTCAAGTTGATGAGGTCAATTAACAGATCCA 922
QY 1046 TGGGATATTTCAAGGGGAAATTAATGTTGGAA 1077
DB 923 TTGGTTTGTATCATGATAGTACTTAGGGGA 954

```

RESULT 10
 AAX83876

```

ID AAX83876 strand; DNA; 3471 BP.
XX
XX AAX83876;
AC
XX 09-SEP-1999 (first entry)
DT
XX
DE Bacillus thuringiensis toxin 86B1 (a) encoding DNA.
XX
XX Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
KW Bacillus corn borer; black cutworm; ss.
XX
XX Bacillus thuringiensis.
XX
XX MO9393991-A2.
XX
XX 08-JUL-1999.
XX
XX 15-DEC-1998; 98WO-US026585.
XX
XX 31-DEC-1997; 97US-00002285.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Schepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI Muller-Cohn J;
PI
DR WPI, 1999-405513/34.
DR P-PSDB; AAT24959.
XX
XX
XX Method for control of European corn borer using Bacillus thuringiensis
XX toxins.
XX
XX Example 5; Page 90-92; 174pp; English.
XX
XX
XX A method has been developed for the control of European corn borer
XX (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
XX amount of a Bacillus thuringiensis toxin. The method is used for the
XX control of European corn borer (Ostrinia nubilalis). The method can also
XX be used for the control of other non-mammalian pests, particularly black
XX cutworm, and other lepidopteran pests. The present sequence encodes a
XX Bacillus thuringiensis toxin from the present invention
XX
XX
XX Sequence 3471 BP; 1144 A; 591 C; 734 G; 1002 T; 0 U; 0 Other;
SO
Query Match 8.0%; Score 172.4; DB 2; Length 3471;
Best Local Similarity 54.2%; Pred. No. 3,4e-31;
Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;
QY 287 GGGAAATCACTCTCGGATATAGTAACTATTGGGACATACCTTAATACATTTCTGCTAGAC 346
DB 158 GCGATGACGAAAAAGAGAGATCTATTGGGCAACACATAGTCTCTTATCACAGCAC 217
QY 347 CCGGATAGGTGGAATTCCTGTATATTTT-----CAATATATTAACAACATCATTCCGT 400
DB 218 CTTCTCTTACTGATTAATTTCAATAGTATATAGCCTTAATAGGTAAGTACTAGAGGTA 277
QY 401 CTTCTGCTCAATCTGTGGACGACCTTCTATATGTGATTTAGTATCTATATTCGTAAG 460
DB 278 GTAGTGACAAATCATAATCAGATTGTCTATATGTGACTTATATCTATATGATTTAC 337
QY 461 AGGTAGACGAGAGGTGTTAGTACGCGGCTGACATTTTGGAGGTAAGTACATGCTT 520
DB 338 GGGTAAGTCAAGATGTTTAAATGATGAGATGAGATTTTAAATGTTCTGTACTCTTAT 397
QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATGGCTTACAGATA 565
DB 398 ACAGGAATCTATTAGAGGCTCTGATAGCTGAATTAAGATCTTAATTCGCTTCTGCTG 457
QY 566 AATCAAAATCTTAAAAAATTGCTGACGTAGTAAACGTTCCAGACGCGGAAGAAGATT 625
DB 458 AAGAACTCCGCTACTCGTTTAAATGCGCCGACTCAGAAATTTGATAGATTTTAAACCGAG 517
QY 626 TCACATAACTTTTAGAGGCTATTAACAGACAGAAAGCTGAATTAATTAATTTGCTTA 685

```

```

Db      518 GGTCTTTACGAATGCGCTCCCTTACGTACACAAATGCCAAATTTATTTACTCTT 577
Qy      686 CGTATGTGCAAGCTGCAAAATGTCATTATTACTATTAAAGGACGATTAAATATAAA 745
Db      578 CTTTGGAGGGCTGCATTTTTCATTATTACTATTAAAGGACGATTAAATATAAA 637
Qy      746 AAGAAATGGGACTGTGTGTCACCGCTTGTATCCAGGCTCAGGAGAACTGATTGTACG 805
Db      638 CTAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
Qy      806 AGCGGTTAAAAGCAAAATATAAGATATATAATTATTTGTTAGGGGTGATATAACAG 865
Db      683 CAAACTAGTAGAGCTTATTGAATCTATATATCTGATTTTGGTACATTGGTATATAGAG 742
Qy      866 GTTTAGATCAGATTAAGACAGGCGGCTCAAGTGTGTAAGTTGGTCCAAATTTATAAAT 925
Db      743 GTTTCACGAACCTAAGCAACGAGGCACTGTGTACAGCTTGGTTGAATTTCAATGAT 802
Qy      926 TTGCTAGGAATGACGTTGGCGGTATTTGATTTATTTGCTATATTTTCCAACTTATGAT 985
Db      803 ATCGTAGAGATGACATTTGATGATTTAGATATAGATGATCAATTTTCAAGTCTGTATA 862
Qy      986 TTGAAAATATATCCATTAGCAACAGTATAGAGTAACTAGAGGAAATTTATACAGATCAG 1045
Db      863 TTACTAATTTACCATTAAGAAACAGATTTTTCAGTTGAGAGGCTCATTTATACAGATCAA 922
Qy      1046 TGGGATATTCAGGGGGAATTAATGTTGGGAA 1077
Db      923 TTGGTTTGTATCATCTGATAGTCTTAGGGGA 954

```

RESULT 11

AA02478 standard; DNA; 2407 BP.

AA02478;

29-AUG-2001 (first entry)

B. thuringiensis DNA encoding a toxic crystal protein, CryET60.

Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
sugarcane; tobacco; kapok; flax; potato; barley; turf grass;
pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
cotton leaf perforator; CryET60; ds.

Bacillus thuringiensis.

Key Location/Qualifiers

1. 2406

/tag= a

/product= "CryET60"

/partial

/note= "No stop codon"

MO200119859-A2.

22-MAR-2001.

13-SEP-2000; 2000MO-US025361.

15-SEP-1999; 99US-0153995P.

(MONS) MONSANTO CO.

Baum JA, Chu C, Donovan WP, Gilmer AJ, Ruper MJ;

WPI; 2001-281518/29.

P-PSDB; AAU02035.

XX

```

PT      Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT      and the polynucleotides that encode them, useful for increasing the
PT      insect resistance of plant.
XX      Claim 17; Page 127-128; 173pp; English.
XX
CC      The sequence encodes a B. thuringiensis Lepidopteran-active delta-
CC      endotoxin, crystal protein CryET60. The Lepidopteran-active B.
CC      thuringiensis delta-endotoxin polypeptides may be used as compositions
CC      that are applied to plant crops to protect them from insect damage. The
CC      polynucleotides may be used in the production of transgenic plants that
CC      express the insecticidal polypeptides and consequently have improved
CC      insect resistance compared to non-transformed plants. Monocyledonous or
CC      dicotyledonous plants may be protected in this way, for example corn,
CC      wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC      tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC      fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC      cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC      cotton leaf perforator and spruce budworm) may be affected by application
CC      of the insecticidal polypeptides (full details given in specification)
CC
SQ      Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;
Query Match      7.6%; Score 162.8; DB 4; Length 2407;
Best Local Similarity 53.4%; Pred. No. 6.3e-29;
Matches 434; Conservative 0; Mismatches 342; Indels 36; Gaps 3;
Qy      287 GGGAAATCAGCTCGGATATAGTAACTATTTGGACATATCTTATATACATTTCTGTAGAAC 346
Db      158 GCGATGACGAAAGAAAGACGATATCTTATTTGGACACATATGCTCTTATACAGCAC 217
Qy      347 CCGGATAGGTGGAATTCCTGATATATTT-----CAATATATAACAACTCATTCGT 400
Db      218 CTCTCTTACTGATTAATTTCAATGATATATAGACCTTATAGGAAAGTACAGAGATA 277
Qy      401 CTCTGCTCAATCTGAGGACGACCTTTCTATATGATTTAGATCTATATTTGCTAAG 460
Db      278 GTAGTGACAAATCATATCAGATTTGCTATATGATGCTTATATATATATGATTTAC 337
Qy      461 AGGTAGACGAGCGGTATAGTACCGGGGTGACATTTTGAAGGGGAATGACTCTT 520
Db      338 GGGTATGCTCAGATGTTTAAATGATGAGATTTGCAATTTAAATGTTCTGACTCTTAT 397
Qy      521 ATCAATATATATCTTC-----ATTATCTTGAGATTTGCTTACAGATA 565
Db      398 ACAGAACTATTTAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
Qy      566 AATCAATCTTAAAAAATTGCTGAGTATTAACGTTTCAAGCAGGGAAGAGATT 625
Db      458 AAGAACTCCGCTACTGTTTGAATGCGCCAGCTCAGAAATTTGATGATTTTAAACCGGAG 517
Qy      626 TCACTAACTTTAGAGGCTCATATCAAGACGAAAGTGAATTTATTTGCTTA 685
Db      518 GGTCTTTAAGAAATGCTGCTGTTAGCTAGCAAAATGCCAAATTTATTTACTCTT 577
Qy      686 CGTATGTGCAAGCTGCAAAATGTCATTATTACTATTAAAGGACGATTAAATATAAA 745
Db      578 CTTTGGAGCGCTGCATTTTTCATTATTACTATTAAAGGACGATTAAATATAAA 637
Qy      746 AAGAAATGGGACTGTGTGTCACCGCTTGTATCCAGGCTCAGGAGAACTGATTGTACG 805
Db      638 CTAATTTGGGGCTATACAAATGCTACACCTTTTATA-----ATTATCAAT 682
Qy      806 AGCGGTTAAAAGCAAAATATAAGATATATAATTATTTGTTAGGGGTGATATAACAG 865
Db      683 CAAACTAGTAGAGCTTATTGAATCTATATATCTGATTTTGGTACATTGGTATATAGAG 742
Qy      866 GTTTAGATCAGATTAAGACAGGCGGCTCAAGTGTGTAAGTTGGTCCAAATTTATAAAT 925
Db      743 GTTTCACGAACCTAAGCAACGAGGCACTGTGTACAGCTTGGTTGAATTTCAATGAT 802
Qy      926 TTGCTAGGAATGACGTTGGCGGTATTTGATTTATTTGCTATATTTTCCAACTTATGAT 985

```

QY	DB	Sequence	Score	DB ID	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	DB	803 ATCGGAGAGAGATGACATTGATGGCATTAGAAATAGTAGCATCATTTTCAAGTCTTGATA	862							
QY	DB	986 TTGAAAAATATCCATTAGCAACAAGTGTAGAGTTACTAGGGAAATTTATACAGATCCAG	1045							
QY	DB	863 TTACTAAATATACCCATATAGAAACAGATTTTCAGTTGATGAGGAGTCAATTATACAGATCCA	922							
QY	DB	1046 TGGGATATTCAGGGGAAATTTATGGTTGGGA	1077							
QY	DB	923 TTGGTTTGTACATGTCGTAGTGTCTTGGAGGA	954							
QY	DB	12 AEA61394 standard; DNA; 4391 BP.								
QY	DB	AEA61394								
QY	DB	AEA61394								
QY	DB	11-AUG-2005 (first entry)								
QY	DB	Bacillus thuringiensis Cry19Aa coding sequence, SEQ ID 4.								
QY	DB	Insecticide; crystal protein; Cry19Aa; gene; db.								
QY	DB	Bacillus thuringiensis.								
QY	DB	Key Location/Qualifiers								
QY	DB	CDS 719..2665								
QY	DB	/tag= a								
QY	DB	/product= "Cry19Aa"								
QY	DB	US2005124803-A1.								
QY	DB	09-JUN-2005.								
QY	DB	30-AUG-2004; 2004US-00929754.								
QY	DB	29-AUG-2003; 2003US-0498826P.								
QY	DB	(OHIS) UNIV OHIO STATE RES FOUND.								
QY	DB	Dean DH, Abdullah MA;								
QY	DB	WPI; 2005-417057/42.								
QY	DB	P-PSDB; AEA61393.								
QY	DB	EMBL; Y07603.								
QY	DB	New modified Bacillus thuringiensis insecticidal crystal proteins (i.e. Cry4Ba and Cry19a) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.								
QY	DB	Disclosure; SEQ ID NO 4; 63bp; English.								
QY	DB	The present invention relates to modified insecticidal Bacillus thuringiensis crystal proteins Cry4Ba and Cry19Aa which have enhanced toxicity against a variety of insects, e.g. mosquitoes and lepidoptera. The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. The present sequence is the coding sequence of the wild-type Cry19Aa protein, which can be modified with: a substitution of amino acids at positions 355 through 358 with amino acids tyrosine, glutamine, aspartic acid, and leucine; an insertion of at least one amino acid (e.g. arginine) after position 358 and a deletion of the amino acids at positions 414 through 418.								
QY	DB	Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;								
QY	DB	Query Match 6.2%; Score 133.6; DB 14; Length 4391;								
QY	DB	Best Local Similarity 48.1%; Pred. No. 9e-22;								
QY	DB	Matches 720; Conservative 0; Mismatches 704; Indels 74; Gaps 9;								
QY	DB	666 TGAATATATATATATGCTACGATATGTCAGCTGCAAGTGCATTTATTTACTATTAAAG	725							

D	1303	TGA	ACTTACTTTTATTCGCTGCTCTATGCAAAATTGCCAATCTGCATTTACTTTATTACG	1362
Q	726	GA	CGAGTTAAATATATATAAAAGAATGGGGACTAGTGTGTCACCGTTGATCCAGGGTC	785
D	1363	GGAT	GCTCAGATTTATGGAAGATTAATGATGGAGCGACG-----AGCTAA	1407
Q	786	AGG	AGAACTGATTTGTATACGACGGTTAAAGCGAAAAATAAAGATATACTAATTATTTG	845
D	1408	TGCT	CGGATATATTAACCAATACAAATTAGAAAAACAAGAAATATACAGATATTGG	1467
Q	846	TGT	AGGGGTATTAACAAGGGTTAGATCAGATAGAAGAGCGGGTCAAGTGTGAAGT	905
D	1468	TAT	AATTTGGATTAATAAGGTTAAATGATTTAGAACAGCAGTCAA-----	1516
Q	906	TTGG	TGCAATTTATATTAATTTCTGTAGAAATGACGTGGCGTATTTGATATTATTTGC	965
D	1517	-TGG	GTAACTTTATCGTATCGTATCGTAGAAATGACTTATCTGTATTAGTATTATTTCC	1575
Q	966	TAT	ATTTCCACTTATGATTTTGAAAAATATCCATTAGCAACAAGTGAAGTTAATTAG	1025
D	1576	AAT	GTCCCTATTTATGACCGGAGATTATCTTACGAAGATTAATAAACCGAATCTACAG	1635
Q	1026	GGA	ATTATACAGATCCAGTGGATTTTCAGGGGGAAATATAGGTTGGGAACGGTTTTT	1085
D	1693	TTCT	TTTGAGAAAGCTGATACCTTTATACAAAGGACCCCATCTCTTCACTTGGCTTAA	1752
Q	1146	AGCT	ATAGATATATATATAGTCACTTCTTATTAATCTTCAGTTGGTATCTTAAGTGGCTGGG	1205
D	1753	AGG	ATTCGATTTGTAACCAATCTTATTTCTTATTGACATTTTATCAGGTGCTCAAA	1812
Q	1206	GGGA	CTCGATATATGAGACTTCAAAAGGGTAAGGTCCTTTCAAGTATGTCTGG	1265
D	1813	TAA	GATTTCTTATACTATATTAATTTCTAGTATTAAAGAGGGCTCTTTAGGGGACAGACAC	1872
Q	1266	AACT	ACGATATATATCCACGTAATATTATTTT---GGCAATACCGATATATTTAAAT	1322
D	1873	AGAT	TATATGGTGGACTTCTTCTACATTAATATTCATCAAAATCGATATGATATTAATTT	1932
Q	1323	TAT	TTCATTAGCTATGATATGCAATGCAACGGTTGTGGTATTTCA--ATCCACGGCA	1379
D	1993	ATGA	CGAAATATATGATATATTATTTATCTTGGGGTGATCTCTTAATATTAATAAAAT	1992
Q	1380	TCT	GTTTCAAGTCAAAATTTTTCGCAACAACATAATCTTCCGTATGAGATTA	1439
D	1993	GAAT	TTTTCTGTAAACGATTAATTAATCTTCAAAAGAAATTAATTTATGCTGACACAGAAC	2052
Q	1440	CAG	TTCTGGTACTACAGACAATTTGATCTGTATACGAGTATTAATAGATCTTACC	1499
D	2053	GAAT	TAACTTGTGGACAGATTTTGATTTTCTACTATATTAAGGGAATGAGTT	2112
Q	1500	ACCT	AGTCGTAACAATTACTCTCATAGATTATCAATATGCGGACATGTGTTCAAA-----	1553
D	2113	AGCA	AAATATATGATTAATCATTAATTTATCTCATATGTATTAATATGAGGAACGTT	2172
Q	1554	---	TGAACCTTCAGAGTTAACGATTTGGTTGGACACATCAAGTATGAAAAAGATTA	1610
D	2173	TGG	TACAGAAACGTCAATGGTATTTGCTTTTACACATATGTATGTATCTCTAATTA	2232
Q	1611	TGAA	TTATTCACAGTAAATTTAGCGAAATCTCGCAGTAAACGTTTGGCCATCCAGC	1670
D	2293	ATCA	TTTCAATGAAAAAGTT-----CCGGATTTACGGAGGAGATTT	2333
Q	1671	AGTA	CAGATATGACAGAGTTACGTCACAGCTGGGCTTGTTATACAGAGAGATGT	1730
D	2293	ATCA	TTTCAATGAAAAAGTT-----CCGGATTTACGGAGGAGATTT	2333
Q	1731	AGTA	ACGTTATCAAGCAAGTTAAAAATACGTTTAACTTTCTGACCCACGAATTA	1799
D	2338	GGTA	AAAGTATGACAGATTCAGGTTTAACTATACGTTTAACTGAAATTTATAGATA	2397

```

QY 1791 AAATTACCGTGTGACTTGCCTACGGAGTGGAGACCTGGTCCGAGTAGAAG 1850
DB 2398 AAAATATCGTGTGGAATACGTTTAAATGTAACAGTTCATAATTAATACGAAA 2457
QY 1851 ATGG---TCGCCAGGTCGTGTTTCAAAATGCTAATTTTCTGTCAGTCAAGGTGCTA 1907
DB 2458 ATGGAAGGGGAGAGGTATATATCAACAACAATTCACAAATTTTCTCCACATATGAGC 2517
QY 1908 TAGTTCATTTGATTTATGACACCTTATGTTACTTATTAATCAATCAGGTGTTGAAT 1967
DB 2518 CTTTCTTATTTAAGCTTTTATCTATTAATACGACGAGAAATATATGATTTGACAAAT 2577
QY 1968 AATTATACAAATTTATCTGTTGTTACCACTTATTTGTTGACAAAGTCGAATTTCCAAAT 2027
DB 2578 GGAAGTAAACATATCTGATATGTTGATGACAGTTTGTGGAAGATATACATCTTATATATGA 2637
QY 2028 TGACATCCAAATTTGAAAATATGTAAGAAATGTCATTTGGAAGAGACATATGATGTA 2087
DB 2638 TAAATGGAATTCCTCCCACTAATGATACATTCACA-----GGAAATATGTA 2686
QY 2088 AGGAGTCAATTCCTTGGAAACAAAAGAGATTTGTAATTTTATTCATTTAA 2145
DB 2687 GGAATAATATGAAATTAAGAAATGACAGAAACATTTAATATGATATTTGTTGATTTAA 2744

RESULT 13
AAS02466
ID AAS02466 standard; DNA; 1959 BP.
AC AAS02466;
XX
XX 29-AUG-2001 (first entry)
DE B. thuringiensis DNA encoding a toxic crystal protein, CryET43.
XX
XX Delta endotoxin; lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET43; ds.
XX
XX Bacillus thuringiensis.
OS
XX
XX Key Location/Qualifiers
FT CDS 1. 1959
FT /tag= a
FT /product= "CryET43"
FT /partial
FT /note= "No stop or start codon"
XX
XX MO200119859-A2.
XX
XX PD 22-MAR-2001.
XX
XX PF 13-SEP-2000; 2000MO-US025361.
XX
XX PR 15-SEP-1999; 99US-0153995P.
XX
XX (MONS ) MONSANTO CO.
XX
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ,
XX
XX WPI: 2001-281518/29.
XX
XX P-RSDB; AAU02023.
XX
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
XX PT and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 17; Page 105; 173pp; English.
XX

```

```

CC The sequence encodes a B. thuringiensis lepidopteran-active delta-
CC endotoxin, crystal protein CryET43. The lepidopteran-active B.
CC thuringiensis delta-endotoxin polypeptides may be used as compositions
CC that are applied to plant crops to protect them from insect damage. The
CC polynucleotides may be used in the production of transgenic plants that
CC express the insecticidal polypeptides and consequently have improved
CC insect resistance compared to non-transformed plants. Monocotyledonous or
CC dicotyledonous plants may be protected in this way, for example corn,
CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification)
XX
SQ Sequence 1959 BP; 646 A; 348 C; 393 G; 572 T; 0 U; 0 Other;
Query Match 5.6%; Score 119.8; DB 4; Length 1959;
Best Local Similarity 55.0%; Pred. No. 1,5e-18;
Matches 294; Conservative 0; Mismatches 217; Indels 24; Gaps 2;
QY 561 AGATTAATCAAAATCCTTAAAACTTGCTGACGTTATTAACAGTCCAAAGCAGGAGAGA 620
DB 411 AGATTAACCGAATGATGCAAGATCAAGACATTAATCTTGAGCGCTATGCTTTAGA 470
QY 621 AGATTCACCTAACTTTAGCAGGCTCATTTACAGACAGAAAGCTGAATATATATAT 680
DB 471 ACTTGACATTAACATGCTATACCGCTTTTACAGAAATGAGAAAGACTTCATTTAT 530
QY 681 GCCTACGATATGTCGAAGCTGCAATGTGCAATTTATTAATTAAGGAGCGCACTTAAATA 740
DB 531 AATGTAATATGCTCAAGCTGCAATTTACACTATTTATTTAGAGAGACGATCCCTTTT 590
QY 741 TAAAAAAGATGGGAGCTAGTGTGTCACCGTGTATCCAGGTCAGGAGAACTGAT 800
DB 591 TGGTAGTAATGGGGAGTGCATCTTCGATTTAACCA-----TA 632
QY 801 TAAAGAGCGGTAAAGCGAAATTAAGATTAATTAATTTAGTGTAGGTGTATTA 860
DB 633 TTACCGAAGAAATGATGATATACAGAGAAATTTCAACATTTGGTACAAATGATTA 692
QY 861 CAAGGTTTATGATCAATTAAGACAGGCGGTACAGTGTGTAAGTTGGTCAATTTAA 920
DB 693 TACAGGCGCTAAATTAATTAAGA-----GGGACAAATGCTGAAGTGTGGCGTATTA 746
QY 921 TAAATTCGTAGAGAAATGACGTTGGCGGTATGATATTAATTTGCTATATTTCACTTA 980
DB 747 TCAATTCGTAAGACCTTAAGTTAGGAGATTAATTAATTAATTTCCCAAGCTA 806
QY 981 TGATTTGAAAAATATCAATTAAGCAACAAGTGTAGATTAACTTAGGAAATTTATACAGA 1040
DB 807 TGATCTCGACCTTAATCAATTAATTAAGAGTGTCTGATTTACAGAGAAATTTATACAGA 866
QY 1041 TCCAGTGGGATTAATCAAGGGGAAATTAATGTTGGAAACGTTTATGCTTTAAT 1095
DB 867 TCCATTTGGGAGAAACAATGACCTTACAGGATTTGCAAGTGAATGTTTAAAT 921

RESULT 14
ADR89411
ID ADR89411 standard; cDNA; 1986 BP.
XX
XX ADR89411;
XX
XX 18-NOV-2004 (first entry)
DE AXMI-009 alternative start site coding sequence #2.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX

```


pesticidal activity.
 XX Bacillus thuringiensis.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2016
 FT /tag= a
 FT /product= "Alternative AXMI-009"
 XX
 XX WO2004074462-A2.
 XX
 XX 02-SEP-2004.
 XX
 XX 20-FEB-2004; 2004WO-US005829.
 XX
 XX 20-FEB-2003; 2003US-0448632P.
 XX 20-FEB-2003; 2003US-0448633P.
 XX 20-FEB-2003; 2003US-0448797P.
 XX 20-FEB-2003; 2003US-0448806P.
 XX 20-FEB-2003; 2003US-0448810P.
 XX 20-FEB-2003; 2003US-0448812P.
 XX 19-FEB-2004; 2004US-00781979.
 XX 19-FEB-2004; 2004US-00782020.
 XX 19-FEB-2004; 2004US-00782096.
 XX 19-FEB-2004; 2004US-00782141.
 XX 19-FEB-2004; 2004US-00782570.
 XX 19-FEB-2004; 2004US-00783417.
 XX
 XX (ATHE-) ATHENIX CORP.
 XX
 XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX WPI; 2004-635574/61.
 XX P-PSDB; ADR89410.
 XX
 XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 XX Claim 1; SEQ ID NO 21; 178BP; English.
 XX
 XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxin of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX
 XX Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;
 SQ
 Query Match 5.5k; Score 118.4; DB 13; Length 2016;
 Best Local Similarity 51.3k; Pred. No. 3.3e-18;
 Matches 544; Conservative 0; Mismatches 426; Indels 90; Gaps 8;
 QY 661 AAAGCTGAATATTTATTTATTTGCTACCTATGTCGAACTGCAATGTGATTTATTTCTA 720
 DB 550 AACTTGAATTTTATTTGTTACCGATATATGCAACCCGCAATTTTGATTTAATTTTA 609
 QY 721 TTAAGGAGCCAGTAAATTAATAAAGAAAGGAGGAGTGTCTCCACCGTTGTATCCA 780
 DB 610 TTAAGAGATCTGATTTATTTTGGAGCAAGTGGCAATTAAGTGTATGAT----- 657
 QY 781 GGGTCAGGAGAACTGATTTGTAACGAGCGGTAAAGCAAAATTAAGAGATATTAAT 840
 DB 658 -----GAAATGTGTGATTAATTAATCAAGACTCAAGAGACTGATTAAGATTAAGAT 711

QY 841 TATTTGTAGGCTGATTAACAAAGGTTTAGATCAGATTAAGACAGCGGTTACAGTCT 900
 DB 712 CATTTGATTAACATTTCTATTAACAGAGGTTTAAATCAATTTATTC-----GCTCAATGCT 765
 QY 901 GAAGTTTGTGCAAAATTTAATAATTTCCAGAGAAATGACGTTGGCGGTATTTGATATT 960
 DB 766 CAAGATTGGGTGAGCTTTAATAGTTTGTGAGAAATATGACATTAACAGATTAAGATCTC 825
 QY 961 ATTGTAATTTTCCAACTTATGATTTTGAATAAATATTCATTTACCAACAGTATAGATTA 1020
 DB 826 GCAATATATTTTCCAACTATGATTCACCGATGATTCATTTACAGAAAAAGCAATTC 885
 QY 1021 ACTAGGAAATTTATACAGATCCAGTGGGATATTCAGGGGAAATTAATGTTGGAAACG 1080
 DB 886 ACTAGGAAATTTATACAGATCCAGTGGGATTTACTGGGGATTAAGAAATGAGATGAG 945
 QY 1081 TTTTTT-----AGTTTATTTCCGTTAGAAAGCAATTTGACCA 1116
 DB 946 ACTTACCTTTGTATTAATCTTAATTAATACAACTTTATCTATGAAATTAACGAAAG 1005
 QY 1117 CGGGACCTGTTAGTACTTGGCTTCAAGCTATAGATATATATATGTCATTTCTATTAAT 1176
 DB 1006 CGAGCTCTTCTTATACCACTTGGCTTAATCTATTTTGTATATACAGAGACTCTAGT 1065
 QY 1177 CTTCAGCTTGTATCTTATAGTGGCTGGGGGAACTGTCATTAATGAAAGCTTACAAAG 1236
 DB 1066 AATATGCTGATGAGAAATATTTGGGGAGGCAATCATTAATGTTGAAATGAAATGAT 1125
 QY 1237 GGTACGGTCTTTTCAAGCTATGCTGAACTACAGATTAATATTCACGCT---AATATT 1293
 DB 1126 GGTTCGAATTAACCAATTAATTTGTAATTAATTAATTAATTAATTAATTAATTTT 1185
 QY 1294 ATTTTGGCAATCCAGATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1347
 DB 1186 AATTTTGGCAATCTTTCTGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1245
 QY 1348 CAACCGTTTGGTGGATTAATCAATCCAGCGCATCTTGTTCACGTCAGAAATTTTCCG 1407
 DB 1246 ACAGAGGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1305
 QY 1408 ACAACACTAATTA-----CTTTCCTATGAGTAAACAGTTTGGGATCTCA 1455
 DB 1306 TCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1365
 QY 1456 CAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1515
 DB 1366 CAAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1422
 QY 1516 TACTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1557
 DB 1423 TTACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1482
 QY 1558 ACTTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1617
 DB 1483 ATTTGATGCTTTTAAAGTTTGGTGGGCAATTAATTAATTAATTAATTAATTAATTAAT 1542
 QY 1618 TATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1657
 DB 1543 GAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1582

Search completed: December 19, 2005, 05:54:17
 Job time : 871.297 secs

1919-1920

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:54 ; Search time 5744.73 Seconds

(without alignments)
17469.639 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145

Sequence: 1 ttccaccaataatgattt.....atagttatttcaatga 2145

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	65.2	3.0	1101	CNS0039G	AL063921 Drosophila
C 2	56.2	2.6	1101	CNS0182P	AL108811 Drosophila
C 3	54.6	2.5	1225	CNS0161D	AL106171 Drosophila
C 4	53.6	2.5	1101	CNS00001	AL065414 Drosophila
C 5	53.4	2.5	1101	CNS0039G	AL063921 Drosophila
C 6	53	2.5	1101	CNS0100X	AL068379 Drosophila
C 7	51.8	2.4	1204	CNS016E2	AL06628 Drosophila
C 8	50.6	2.4	928	CNS0102F	AL068433 Drosophila
C 9	49.8	2.3	944	CNS002K1	AL068220 Drosophila
C 10	49.6	2.3	1101	CNS00E5I	AL069797 Drosophila
C 11	48.8	2.3	938	CNS009E1	AL063529 Drosophila
C 12	48.4	2.3	938	CNS006TJ	AL065906 Drosophila
C 13	48.2	2.2	1101	CNS0106X	AL068379 Drosophila
C 14	48	2.2	663	CNS01008	AL068595 Drosophila
C 15	47.2	2.2	1101	CNS00100	AL068595 Drosophila
C 16	46.6	2.2	867	CNS075E6	AL068607 Drosophila
C 17	46.6	2.2	1146	CNS021G2	AL429890 clone BAO
C 18	46.6	2.2	1193	ALJ926097	AL176843 Tetraodon
C 19	46.4	2.2	443	CNS08293	ALJ926097
C 20	46.4	2.2	572	CNS08293	ALJ926097
C 21	46.4	2.2	749	CNS08293	ALJ926097
C 22	46.2	2.2	554	CNS08293	ALJ926097

23	46	2.1	355	1	AA448356	AA448366 zw96c06.1
24	46	2.1	511	6	CB158772	CB158772 K-BST0218
25	46	2.1	817	5	BU773209	BU773209 SUBFID12
26	46	2.1	1414	4	BC025177	BC025177 Homo sapi
27	46	2.1	7050	10	AY420513	AY420513 Homo sapi
28	45.8	2.1	456	3	BJ390240	BJ390240 BJ390240
C 29	45.8	2.1	764	9	BZ025901	BZ025901 oeh92B02.
C 30	45.8	2.1	1101	10	CNS003B6	AL064084 Drosophila
C 31	45.8	2.1	1225	8	DN671106	DN671106 CFM60-G08
C 32	45.8	2.1	1296	10	AG350007	AG350007 Mus muscu
C 33	45.6	2.1	698	9	BH940466	BH940466 ood80904.
C 34	45.6	2.1	811	10	CZ534216	CZ534216 SRAA-aac8
C 35	45.4	2.1	347	3	BJ399104	BJ399104 BJ399104
C 36	45.4	2.1	858	8	DR732187	DR732187 FCAS07810
C 37	45.4	2.1	982	10	CNS001T8	AL075613 Drosophila
C 38	45.4	2.1	1101	10	CNS017X8	AL108171 Drosophila
C 39	45.2	2.1	350	10	N97363	N97363 0356M7 gmbp
C 40	45.2	2.1	583	9	BH725336	BH725336 BOH043TR
C 41	45.2	2.1	1073	1	AJ928975	AJ928975 AJ928975
C 42	45.2	2.1	1099	10	CNS00DW8	AL076311 Drosophila
C 43	45	2.1	572	11	CR332988	CR332988 mcel-62N1
C 44	45	2.1	581	8	DN470449	DN470449 USDA-EP 1
C 45	45	2.1	581	8	DR755050	DR755050 USDA-EP_1

ALIGNMENTS

RESULT 1
LOCUS CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08X10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921 GI:4941778
VERSION GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutyo Oosawa and Aaron Mammoe in Pletier de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08X10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 1225)
Ephyrtoidea: Drosophilidae; Drosophila.
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source
Location/Qualifiers

1..1225
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15C18"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN

Query Match 2.5%; Score 54.6; DB 10; Length 1225;
Best Local Similarity 25.3%; Pred. No. 0.05;
Matches 199; Conservative 164; Mismatches 415; Indels 5; Gaps 1;

110 TAAAGACTATATAGAGGAGTAAATATGATTTCTTATCAAAATACAAATGATATGAA 169
1210 TTTTATATTTTAAAT 1151
170 TTTCGATGATGATCCCGAATACCAATATATGCAACAGATATCCCTTGGCAAGATC 229
1150 TTTTAAATATTTTAT 1091
230 CAATATATTTCTAT 289
1090 TAAATATATTTTAAAT 1031
290 AATCAGTCTGAT 349
1030 TTTTATTTTAAAT 971
350 GTATAGTGAATTCCTGTAATA-----TTTCAATATATATATATATATATATATAT 404
970 TTTATTTAAATTTTAAATATATATATATATATATATATATATATATATATATAT 911
405 TGATCAATCTGTGACAGCACTTTCTATATATATATATATATATATATATATATAT 464
910 RTTAAAT 851
465 AGACGAGAGCGGTAAAGTACCGGGTTCAGATTTTGAAGGTAATGACCTGTAATCA 524
850 TTTTATTTTAAAT 791
525 AGATATATATCTGAT 584
790 ARAAAMDDTTWNTKKTATTTTATATATATATATATATATATATATATATATATAT 721
585 TGATGATGATTTTAAAGTTCAGAGCAGGAGAGATTTTCAATATATATATATATAT 644
730 WTDTDAAT 671
645 GTCTATATCAAGACAGAGAGTGAATATATATATATATATATATATATATATATAT 704
670 ANGAKMTAT 611
705 TGTGAT 764
610 ATTAT 551

RESULT 4

CNS00001 1101 bp DNA linear GSS 03-JUN-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TERT3 end of BAC #
BACR01J16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

AL065414 GI:4938827

VERSION

AL065414

KEYWORDS

Drosophila melanogaster (fruit fly)

SOURCE

Drosophila melanogaster

ORGANISM

Drosophila melanogaster (fruit fly)

REFERENCE

Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

AUTHORS

Genoscope.

TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osoegawa and
Aaron Mosmoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR01J16"
/clone_lib="RPCI-98"
/note="end : TERT3"

ORIGIN

Query Match 2.5%; Score 53.6; DB 10; Length 1101;
Best Local Similarity 15.6%; Pred. No. 0.085;
Matches 71; Conservative 199; Mismatches 185; Indels 0; Gaps 0;

813 AAAAGCAAT 872
582 AAT 641
873 TCAGATTAAGACAGCGGATGACAGCTGAAGTTTGTGCAATTAATTAATTTGCTAG 932
642 KKKKRTKGAAT 701
933 AGAATAGAGTGGCGGTATTTGATATATATATATATATATATATATATATATATAT 992

Db 702 AKARAKRWKDKDTKKKTKTTATKTTTAAATDKWKRRKKKATAGAMDMDARRG 761
QY 993 ATATTCATTAGCAACAAGTGTAGTAACTAGGAAATTTATACAGATCGAGTGGA 1052
Db 762 RGRMGDKRRRTARAGKDKTKGKKKTDGRDGGGGDRGDGAGGGDRARARAR 821
QY 1053 TTCAGGGGGAATTTATGTTTGGACGCTTTTATGCTTAATTCGGTAGAACAAATG 1112
Db 822 WDTRDTRGADKADKKKAGKKRMTKTKRPTADMKAMAARWRBRDRRDR 881
QY 1113 AACACGGGACCTGTTTATGTTAGTCTGCTTCAAGTATATATATATGCTTAT 1172
Db 882 WRWRGADKKMKDDDDTADTKDWTATAGTAGMDDDKADGDGMRKGTDMRTKRT 941
QY 1173 TATCTTACGCTGTATCTTATGCTGCTGGGGGGAACCTCGCATTAAGAACTTAC 1232
Db 942 WKMGRRGDKRKTAGRAGDKKKKKDKDRDIDAATGDKDTWDJTDTKRRRRKR 1001
QY 1233 AAAGGTAACGCTGTTTCAACGTATGCTGGA 1267
Db 1002 RRAGRGRDKDKKKRBRARWKKKKTKDKDD 1036

RESULT 5
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR08K10 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL063921 GI:4941778
VERSION AL063921
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoler in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1. 1101
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone_lib="RPCT-98"
/note="end : TET3"

ORIGIN
Query Match 2.5%; Score 53.4; DB 10; Length 1101;
Best Local Similarity 22.3%; Pred. No. 0.095;
Matches 102; Conservative 156; Mismatches 199; Indels 0; Gaps 0;
QY 1 TTTCACCAATATATATGTTTTTTGTAGAAACATTTTACAGAAATCATTTGGGTACTA 60

Db 411 TTTTAAABAAABAAATATTTTAAABAAABAAATTTTAAABAAABAAATTTTAA 470
QY 61 CGAATATATAGAAAGACACCTGGCATATATTTATTTAGTGTCTTAAATTAAGACTA 120
Db 471 AAAAAAAAAAATTTTTTTTTTTTAAATTAATTAATTTTAAABAAABAAABAA 530
QY 121 TAAGAGTGAAGAAATATGAATCTTATCAAAATATGAATGAATGAATCTGATGGT 180
Db 531 AAAAAAAAAAATTTTTTTTTTTTAAATTAATTAATTTTAAABAAABAAATTTT 590
QY 181 TCCCGAATTAACAATATATGTAATGTAATGTAATGTAATGTAATGTAATGTA 240
Db 591 TNNHTTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNN 650
QY 241 CSTATTAACTGAGAGCTTGACAGGAAGGCGATGAGATAGTGGATGAGTCTG 300
Db 651 YNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNHNN 710
QY 301 GATATAGTATGATTTGGGACATACCTTATGAACTCTGATGAAACCGTATAGTGA 360
Db 711 NHTHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNN 770
QY 361 ATTCCGTAAATATTTTCAATATTAACAACATCTCCGTCTTGTCAATCTGTGCA 420
Db 771 HYAAAAAAMAATTTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNN 830
QY 421 GCACCTTCTATATGATTTAGTATCTATTAATCTGTA 457
Db 831 HMMMTTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNNHTNN 867

RESULT 5
CNS0100X 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL098379 GI:5609990
VERSION AL098379
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.biol.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CERH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
source
1. 1101
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03G04"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN
Query Match 2.5%; Score 53; DB 10; Length 1101;
Best Local Similarity 16.2%; Pred. No. 0.12;
QY 1

	CNSL6E2	1204 bp	DNA	linear	GSS 26-JUL-1998
RESULT 7 CNSL6E2/c	LOCUS				
	DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
	ACCESSION	AL106628			
	VERSION	ALI06628.1 GI:5622852			
	KEYWORDS	GSS.			
SOURCE	ORGANISM	<i>Drosophila melanogaster</i> (fruit fly) <i>Drosophila melanogaster</i> Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epmydroidae; Drosophilidae; Drosophila. 1 (bases 1 to 1204)			
REFERENCE AUTHORS TITLE	JOURNAL	Genoscope. Direct Submission			
COMMENT	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre de Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton				

[illegible]

RESULT 8	
CNS0102F/c	CNS0102F
LOCUS	928 bp DNA linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN03B09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL098433
VERSION	AL098433.1
KEYWORDS	GI:5610044
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 928)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

```
1..928
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03B09"
/clone_1ib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"
```

ORIGIN

Query Match 2.4%; Score 50.6; DB 10; Length 928;
Best Local Similarity 21.6%; Pred. No. 0.44;
Matches 121; Conservative 172; Mismatches 268; Indels 0; Gaps 0;

```
470 AGAGCGGTAAAGTGAACGGGTTGCAGATTTCGAGGTAAGTCACTTATCAAGATT 529
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
922 AGAKMGAMGMRWMAATDMWATATWATKAKRWGAGTRWATYAKAKRGAGAKRWAAW 863
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
530 ATTATCTTCATTATCTTGAGATTGGCTTACAGATTAATCAATCTTAAAAAATTGCTG 589
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
862 ATAKAKWGTWGAKKMTADKKDTGGTGTGWTGMRRTKKRGRAGAGGCTGDRTRR 803
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
590 ACGTAGTTAAACGTTCCAAACGCGGAGAGAAGATTCTACTTAACTTTAGCAGGGTCAT 649
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
802 RAKAKRWAKARAKATAMADMGARWMAWMAWDATCATWMAWATATATATATATAT 743
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
650 TATCAAGACAGAAAGCTGAATATTTATTTGCTGCTGTCGCAAGCTGCAAAATGTC 709
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
742 AAMARWRDRRAATGTGKMTGGTTAAAGATKGGMDTRADAKKAAGTTATKTATATG 683
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
710 ATTATTTACTATTAAAGGACGAGTAAATATATATATATATATATATATATATAT 769
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
682 TADBARAKAKMKWKATKAKAGATATPAATGADMGATWGTGKTAGAKTTGTAGWTG 623
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
770 CGTTGATTCAGAGGTCAGGAGAACTGATTGTAAACGCGGTTAAAAAGCAAAATAAAG 829
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
622 RKMTDKWRRTDRDRTAGRRRAATAMGAADDMRDGWRAGTAGRRRMDGMRRAADR 563
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
830 AGTATCTAATTTATTTGTAGGGTGTATTAACAAGGTTAGATCAGATTAAGCAGCGG 889
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
562 TRPAGAADRPAGAAAAAGTGTADADKPAARGKKGDKRKKTGTGAAATGTGWRAGRA 503
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
890 GTACAAGTCTGAAGTTGGTGAATTTATTAATTTCTGAGAGAAATGACCTTGCGCG 949
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
502 KQDDBKRGWKKKRRKAKDKTKTMDPTTDKAKAKATGAKGDKAKRWAGKRRKGGGAG 443
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
950 TATTTGATTTATTTGCTATATTTTCCAACTTATGATTTTGAATAATTCATTAGCAACA 1009
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
442 ATATRTGCMGMDWATTTGATTTATGTATATATKAMAKAGAMTBRAKAKRAAAGCAAA 383
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1010 GTGTAGAGTTAACTAGGGA 1030
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
382 AAKGAGAAKAKRAAAAAA 362
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 944)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

```
1..944
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN02L13"
/clone_1ib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"
```

ORIGIN

Query Match 2.3%; Score 49.8; DB 10; Length 944;
Best Local Similarity 49.5%; Pred. No. 0.69;
Matches 102; Conservative 6; Mismatches 98; Indels 0; Gaps 0;

```
8 AATATTAATGTTTTTTTGTAGAACATTTGTTACAGAAATACATGGGGTACTAGAAAT 67
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
365 AATGAAATGCTAGTATACAAAGCTATATATGCAATATTTGTTAABAGATGCT 424
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
68 ATGAAAGACACCTGGCATATATTTATTTAGTGTCTTAAATAAGACTATATTAAGAG 127
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
425 ATBAAATTAATCTGAAGGCTGTGCTTTGTGTATCAAAACAGAGGCTGATACGCGG 484
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
128 TGAATAATATGTAATTTCTTATCAAAATCAAAATGAATATGAATTTGATGTTCCCCGA 187
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
485 CNGAAAGATTACCTTTATTTATTTAAAGATTAACATTAACATNNATTTATTAAMAA 544
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
188 ATPACCAATATATGTCACAAAGATAT 213
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
545 RAATATCATCTRCMTGAAAAGAGAT 570
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 10

CNS00ES1/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Drosophila melanogaster genome survey sequence TBT3 end of BAC:
BACR29L15 of RPT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069797.1 GI:4949738
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```
1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29L15"
/clone_1lb="RPCL-98"
/notes="end : TET3"
```

ORIGIN

Query Match 2.3%; Score 49.6; DB 10; Length 1101;
Best Local Similarity 21.0%; Pred. No. 0.8;
Matches 112; Conservative 171; Mismatches 250; Indels 0; Gaps 0;

```
Qy 630 TAACTTTTACGAGGTCATTTATCAAGACGAAAGCTGAATATTATTGCTTACGTA 689
Db 1082 KRWMTAKATTAARADGAMGRTGADRWGMDGRTATRAWTADTTGGAGARGRK 1023
Qy 690 TGTGCAAGTCGCAATGCGATTATTAATTAAGGACGACGTAATTAATAAAGA 749
Db 1022 GKDDTATKAGTATATGTTGTTGMDWKKRTATRAAKGATKAKAGATRAKMTD 963
Qy 750 ATGGGAGCTAGTGTGTCACCGTTGATCCAGGTCGAGGAGAACTGATTGAACGACG 809
Db 962 AKDADATKXKMGATGDTTGMAAGRTTGWGTTDDKAGATKTTTGTGATGAGWG 903
Qy 810 GTTAAAGCGAAATTAAGATATTAATTAATTTGTAAGGTGTAACAAGGTTT 869
Db 902 AGAAGKAGMGWGMDAGTRMGWRADTDKGMPTGDKGTGTRWAKTTT 843
Qy 870 AGATCAGATTAAGACGCGGGTCAAGTGCAGGTTTGGCAAAATTTAATAATTCG 929
Db 842 KTRTTATATATATTAADADWAGRKMAATTTTAKATWATATTTAGATGAD 783
Qy 930 TAGAGAAATGACGTTGCGGATTTGATATTTGCTATATTTCCACTTATGATTTGA 989
Db 782 ADADKAGTAGARWAGTATADAKATRTADATTAATGATGCTGKMGKAAAGRTMGMW 723
Qy 990 AAAATATCCATTAGCAACAAGTGTAGATTAACTAGGAAATTTAACAATCCAGTGG 1049
Db 722 RTWDKAARARAGWMAATRRGWARADRWMAAATAATWTGTATWTATTTTGT 663
Qy 1050 ATATTCAGGGGAAATTAATGTTGGGAAAGGTTTGTATTAATTCGGTAGAGCAA 1109
Db 662 DTKTRATATGTTKTKMAKATTTGDDTATTTDRKTTTGTGWDGDDGGRDCKGKGTGA 603
Qy 1110 TGAACAACGGGACCTGTTTACTTACTGCTTCAAGCTATAGATATATATA 1162
Db 602 AATRAARAVGKATKADWMDHTTTTWTCKMTTITKDRTTTGTGRTTTTWT 550
```

RESULT 11
CNS009G1/c 876 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR19J14 of RPCL-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.
ACCESSION AL053529.1 GI:4935018
VERSION AL053529
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 876)
Genoscope.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence ;
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```
1. .876
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19J14"
/clone_1lb="RPCL-98"
/notes="end : TET3"
```

ORIGIN

Query Match 2.3%; Score 48.8; DB 10; Length 876;
Best Local Similarity 44.9%; Pred. No. 1.2;
Matches 83; Conservative 18; Mismatches 84; Indels 0; Gaps 0;

```
Qy 64 ATATATAGAAAGACACCTGCGATATATTTTATAGTGTCTTAAATAAGACTATATA 123
Db 798 ATATATATATATTAATNMAATTAATTAATTAATTTATTAATTAATTAATTAAT 739
Qy 124 GAGTGAATAATATGATTTCTTATCAAAATCAATGATATGAATTCGATGTTCC 183
Db 738 ATWATATATATATATTTTATTAATAATATATATATATATATATTAATTAAT 679
Qy 184 CGAATTAACCAATATGCAACAGATATCCCTTTGCAAGATCCAAATATATTCCT 243
Db 678 WAAATATATATATATATATATATATATATATATATATATATATATATAT 619
Qy 244 ATTA 248
Db 618 WTTTA 614
```

RESULT 12
CNS006TJ/c 938 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR14J11 of RPCL-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.
ACCESSION AL065906
VERSION AL065906
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 938)
Genoscope.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence ;
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooezawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source

Location/Qualifiers
1..938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_11b="BACR14J11"
/note="end : T7"

ORIGIN

Query Match

Best Local Similarity 21.8%; Pred. No. 1.5; DB 10; Length 938;

Matches 84; Conservative 155; Mismatches 148; Indels 2; Gaps 1;

QY 710 ATTATTATCTATTAGGAGCAGTTAATATATAAAGAATGGGACTAGTGTCCAC 769

DB 936 AAKAADATKAAADKADAKADAKAAADAMARADKDKADKADKADKADKADKADKAD 877

QY 770 CGTTGATCCAGGCTCGGAGACTGATTGTAACGCGGTTAAAGCAAAATATAAG 829

DB 876 KAKAKKKKKAKKKKKAKKA--KKAKKKAKKKAKKADAAAKKAKAKAAAWA 819

QY 830 AGTATATAATTTATGAGGGGTGATATAAAGGTTAGATCAGATAGACAGGCG 889

DB 818 DKAAKADADKADAAKADKADKADKADKADKADKADKADKADKADKADKADKAD 759

QY 890 GTACAAGTGTGAGTTGTCGAATTTAATAATTTGAGAGAATGACGTGGCG 949

DB 758 AADAAAKAADRADAAKADAKAAAKAAKAAKADKKADKKAMAMADADNRADK 699

QY 950 TATTGATATTATTGCTATATTCCAACTTATGATTTGAAAATATCCATTGCAACA 1009

DB 698 CAGDKMAADDDKAAKRAAAAMAWMAADADAKATADAKAKAKDKKKDAKAKD 639

QY 1010 GTGTAGATTAACTAGGAAATTTATCAGATCCAGTGGGATATTTCAGGGGAAATTATG 1069

DB 638 KKAARAGAKDKDKDKGTATATKAAAAAKKAKKADTTDTKTWATATDKTIDGWT 579

QY 1070 GTTGGGAACGTTTTTTAGCTTTAT 1095

DB 578 DKATATATRGAKTGKATGTWTTAT 553

RESULT 13
CNS0106X 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL098595.1 GI:5610206
VERSION GSS.
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 1101)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted
JOURNAL BP 191 91006 EVRY cedeX - FRANCE (E-mail : segrete@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBel0BAC11.

FEATURES

Source

Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_11b="DrosBAC"
/plasmid="pBel0BAC11"
/note="end : T7"

ORIGIN

Query Match

Best Local Similarity 19.1%; Pred. No. 1.8; DB 10; Length 1101;

Matches 107; Conservative 227; Mismatches 220; Indels 7; Gaps 2;

QY 487 GGGGTTCAGATTGAGGGTGAATGACTGTTATCAAGATTATATCTTATCTT 546

DB 547 GKGTCGSAKGRITGVKKBKHTHTWYTGKCTCTGKHTTKTTWTTWAKGK 606

QY 547 GAGGATGGCTTACATTAATCAATCTTAAAAAATTGCGAGCTAGTTAAACGTT 606

DB 607 TGTDDAKKATKATGATGATATATATATATATATATATATATATATATATAT 666

QY 607 CAAGCAGGAGAAAGATTCACTTAACTTTAGCAGGCTTATCAAGACAGAAAGCT 666

DB 667 TAKDKMKDKATKAKKAAKAAKAAKAAKATGDKADAKAKAKAKAKAKAKAK 726

QY 667 GAAATATTTATTTGCTTACGATGATGCAAGTGCATAATGTCATTATTTATTA 726

DB 727 TWTATTAADAADK---GAKDKAKAKADADKRWDDKDKRRKAKAKAAADADA 782

QY 727 GAGCAGTTAATATTAATAAAGAAATGSGGACTAGTGTCCACCGTTGATCCAGG 786

DB 783 DAKDAPAAAKAKADADDDRGDGKKRRADKKKKKKDKADWEDKKAK--KDKAA 839

QY 787 GGGAGAACTGATTTGTAACGAGGTTAAAGGAAATAAAGATATCTAATTTAT 846

DB 840 KAKADAAAGAKARRRAGDKADAKADAKAKAKAKADDDAKAATKAKATKAKD 899

QY 847 GTAGGGTGTATTAACAAGGTTTATGATCAGATAGAAGCGGGTCAAGTCTGA 906

DB 900 KKKKKKKDKADAKAKAKADKDDDKDKADKKKWKDRAKDKKADKKDDDKD 959

QY 907 TGCTCGAAATTTATTAATTTGCTAGAGAAATGACGTTGGCGTATGATATTT 966

DB 960 KAKDKDKDKADAKAKAKADADAKAKAKAKADADADADADADADADADADAD 1019

QY 967 ATATTTCAACTTATGATTTTGAATAATTCATTGCAACAAGTGTAGAGTTAG 1026

DB 1020 DDAAKAKADAKADADAKAKAKAKAKADADADADADADADADADADAD 1079

QY 1027 GAAATTTATACAGATCCAGTG 1047

DB 1080 AKAKDAKAKAKAKAKAKKD 1100

RESULT 14
Bj401008/c 663 bp mRNA linear EST 10-MAR-2002
LOCUS Bj401008

DEFINITION Bt401008 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds15e22 3', mRNA sequence.
ACCESSION Bt401008
VERSION Bt401008.1 GI:19333925
KEYWORDS Dictyostelium discoideum
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
AUTHORS 1 (bases 1 to 663)
TITLE Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
JOURNAL Full length cDNA of Dictyostelium discoideum at the slug stage
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..663
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:4689"
/clone="dds15e22"
/sex="mat A"
/dev_stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
ORIGIN
Query Match 2.2%; Score 48; DB 3; Length 663;
Best Local Similarity 56.2%; Pred. No. 1.8;
Matches 99; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 89 ATTATTAGGTGCTTAAATATAGCATATATAGAGTAAATATGATCTATC 148
DB 362 AATATTAGGGGTAAAGATAAACCTGCTGTAATCAAAATTTTCAACCTATG 303
QY 149 AAAATACAAATGATATGAAATTTCTGATGCTCCGAAATACAAATATGTCAAACA 208
DB 302 AATACATGAAGATTAATATATATAGTATATGCTGATACAAATAGTTTATGCCCCAGT 243
QY 209 GATATCTTTTGCAGAGATCAAAATATATTTCTATTAA 248
DB 242 CAATTCCATCTGAAATGATACAAACAGTTCCTTAAA 203
RESULT 15
CNS00100/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR32D23 of RPECI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL068607
VERSION AL068607.1 GI:4958689
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 101 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Oscegawa and
Aaron Mammogher in Plecter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPECI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR32D23"
/clone_lib="RPECI-98"
/note="Tend : TET3"
ORIGIN
Query Match 2.2%; Score 47.2; DB 10; Length 1101;
Best Local Similarity 20.2%; Pred. No. 3.1;
Matches 96; Conservative 158; Mismatches 221; Indels 0; Gaps 0;
QY 792 AACTGATTTGACGAGCGTTAAAGCGAAATATAGATATATATTTGTAGG 851
DB 897 WDWDAAWKKKDKDKTKKKKKGGKAKGAAABADRGAAADBAADBAKTKTKAKTKWK 838
QY 852 GTGTATTAACAAGGTTTATATCATATTAACAAGCGGGGTGACAAAGTCTGAGTGGTC 911
DB 837 KKKGGGWRGTRKGGKGGTRKAGDTKKKKKKKKGGGDKKRTWKTKTKTKTGTGT 778
QY 912 GAATTTAATAATTTGCTGAGAGAAATGACGTGGCGTATGGAATATATTTGCTATAT 971
DB 777 AMTKTGKKKKKKKKKKKKKKDKWTGKTMTKTGKTGSGGKKTKTKGKTWMA 718
QY 972 TCAACTTATGATTTGAAATATATCCATTAGACAACAGTGTAGATTAACTAGGAAAT 1031
DB 717 AMRAKTKTKTKKKKGTAKTADTKKKKKKKDKKTKGKKKTKGKAAWMTGDTRTDKK 658
QY 1032 TTATACAGATCCAGTGGGATATTCAGGGGAAATTTATGTTGGAAACGTTTATGCTT 1091
DB 657 KKAAAMNDTDTDKTKAKKADTADTGKKAATKAKAKAGWADADGDTTKAKTKGT 598
QY 1092 TAAATCGGTAGAACAAATGGAACAGGGGACCGTGTATGTTACTTGCTCAAGCTAT 1151
DB 597 KADDTGKGKAAAGKGGKRTDKGAKGDKATAGAKKTKAKGDAKKGKGRADGG 538
QY 1152 AGATATATATAGTCATTTATTTATCTTCAGCTTGTTATCTTAGTGGCGGGGAAC 1211
DB 537 ARTTRGKKKKAAGTKKDKDKGCTDKGATRTGTGKBRAGKGDGADGTGKGKAGAR 478
QY 1212 TCGCTATATGAAGACTTCAAGGTAACGCTGCTTTCAACGATGCTGGA 1266
DB 477 GKAAAGVAGARTGAGGAGAKRGGTGTRKKAGGAGWGRDAGWGRAKGR 423

Search completed: December 19, 2005, 12:54:26
Job time : 5749.73 secs

11-12-1944

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 05:00:43 ; Search time 7232.94 Seconds

(without alignments)
16857.498 Million cell updates/sec

Title: US-10-782-141-1

Perfect score: 2145
Sequence: 1 ttccaccaataatcaatgttt.....atagttattatcaatcaa 2145Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmb1:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sta:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2145	100.0	2145	6	CQ868324
2	2019	94.1	2019	6	CQ868325
3	2010	93.7	2010	6	CQ868327
4	949.2	44.3	3746	1	AB074414
5	855	39.9	5960	6	CQ868311
6	812.4	37.9	4100	1	AB112346
7	747.2	34.8	2082	6	CQ868312
8	739.8	34.5	2073	6	CQ868314
9	214	10.0	3931	1	AB161456
10	197.2	9.2	2028	1	BTU8188
11	180.6	8.4	2024	1	BTU8188
12	172.4	8.0	3468	6	AR143378
13	172.4	8.0	3468	6	AR567184
14	172.4	8.0	3471	6	BD062618
15	172.4	8.0	3471	6	BD128371
16	172.4	8.0	3471	6	AR205863
17	172.4	8.0	3471	6	AR339971
18	172.4	8.0	3471	6	AR559861

19	172.4	8.0	3726	6	AR143379	AR143379 Sequence
20	172.4	8.0	3726	6	AR567185	AR567185 Sequence
21	172.4	8.0	3837	1	BTCTRYGL	X58534 B.thuringie
22	172.4	8.0	12579	1	BTCTRYI	X58120 B.thuringie
23	162.8	7.6	2407	6	AR359378	AR359378 Sequence
24	162.8	7.6	2407	6	AR359378	AR359378 Sequence
25	147.4	6.9	3668	1	AB18105	AB18105 Sequence
26	133.6	6.2	4391	1	BTJEG65	Y07603 B.thuringie
27	119.8	5.6	1959	6	AR359366	AR359366 Sequence
28	119.8	5.6	1959	6	AX098635	AX098635 Sequence
29	118.4	5.5	1986	6	CQ868322	CQ868322 Sequence
30	118.4	5.5	2016	6	CQ868320	CQ868320 Sequence
31	118.4	5.5	2049	6	CQ868318	CQ868318 Sequence
32	118.2	5.5	3696	1	AY138457	AY138457 Bacillus
33	118.2	5.5	3842	1	BTMCRYIBC	Z46442 B.thuringie
34	118.2	5.5	3934	1	BACCRYIE	L32020 Bacillus th
35	118.2	5.5	3934	6	AR068828	AR068828 Sequence
36	118.2	5.5	3934	6	I38760	I38760 Sequence 3
37	118.2	5.5	3934	6	I70138	I70138 Sequence 3
38	118.2	5.5	8306	1	BTU07026	U70726 Bacillus th
39	117.6	5.5	1806	6	CQ868303	CQ868303 Sequence
40	117.6	5.5	1890	6	CQ868301	CQ868301 Sequence
41	117.6	5.5	2190	6	CQ868300	CQ868300 Sequence
42	116.8	5.4	2549	1	AY570734	AY570734 Bacillus
43	116.8	5.4	3684	1	AF077326	AF077326 Bacillus
44	116.8	5.4	3684	6	I90319	I90319 Sequence 7
45	116.8	5.4	3684	6	AR359400	AR359400 Sequence

ALIGNMENTS

RESULT 1	CQ868324	2145 bp	DNA	linear	PAT 13-SEP-2004
LOCUS	CQ868324	Sequence 25 from Patent WO2004074462.			
DEFINITION	CQ868324				
ACCESSION	CQ868324				
VERSION	CQ868324.1	GI:51998370			
KEYWORDS					
SOURCE					
ORGANISM	Bacillus thuringiensis				
	Bacillus thuringiensis				
	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus				
	cereus group.				
REFERENCE					
AUTHORS	Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.				
TITLE	Delta-endotoxin genes and methods for their use				
JOURNAL	Patent: WO 2004/074462-A 25 02-SEP-2004;				
	Athenix Corporation (US)				
FEATURES					
source	1. 2145				
	/organism="Bacillus thuringiensis"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:1428"				
ORIGIN					
Query Match	100.0%	Score 2145;	DB 6;	Length 2145;	
Best Local Similarity	100.0%	Pred. No. 0;			
Matches 2145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TTTACCAATATATATGTTTTTTTGTAGAAACATTGTTACAGAAATACATTTGGGGTACTA	60		
DB	1	TTTACCAATATATATGTTTTTTTGTAGAAACATTGTTACAGAAATACATTTGGGGTACTA	60		
QY	61	CGAATATATAGAAAGACCTGGCAATATTTATTTAGTGTCTTAAATTAAGACTATTA	120		
DB	61	CGAATATATAGAAAGACCTGGCAATATTTATTTAGTGTCTTAAATTAAGACTATTA	120		
QY	121	TAAAGAGTAAATATGAAATTTCTTATCAAAATACAAATGAAATATGAAATTTGATGAT	180		
DB	121	TAAAGAGTAAATATGAAATTTCTTATCAAAATACAAATGAAATATGAAATTTGATGAT	180		
QY	181	TCCCGAATACCAATATGTCAAACAGATATCCTTTGCAAGAGATCCAAATATATTT	240		
DB	181	TCCCGAATACCAATATGTCAAACAGATATCCTTTGCAAGAGATCCAAATATATTT	240		

Db 181 TCCCCGAATACAAATATGTCAAA CAGATATCTTTTGCAAGATCCAAATATATTT 240
QY CCTATTAACTGGAGCGTTGTGAGGGAAGGCCATGCGAAGATCGTGGAAATACGCTCG 300
Db 241 CTTATTAACTGGAGCGTTGTGAGGGAAGGCCATGCGAAGATCGTGGAAATACGCTCG 300
QY 301 GATATAGTAACTATTGGGACATACCTTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
Db 301 GATATAGTAACTATTGGGACATACCTTTATCAATTTCTTGCTAGAACCCGGTATAGGTGA 360
QY 361 ATTCTGCTAATATTTCATATTAATTAACAACTCATCTTCGTTCTGCTCATCTGTGGCA 420
Db 361 ATTCTGCTAATATTTCATATTAATTAACAACTCATCTTCGTTCTGCTCATCTGTGGCA 420
QY 421 GCACCTTTATATGTATTTAGTATCTATATTCGTAAAGAGTAAAGCGAGCGGTTA 480
Db 421 GCACCTTTATATGTATTTAGTATCTATATTCGTAAAGAGTAAAGCGAGCGGTTA 480
QY 481 AGTACGGGGTTCAGATTTTGGAGGTAATGACTGCTTATCAAGTATTAATCTTCAAT 540
Db 481 AGTACGGGGTTCAGATTTTGGAGGTAATGACTGCTTATCAAGTATTAATCTTCAAT 540
QY 541 TATCTTGAAGATTTGGCTTACAGATTAATCAATCTTAAATCTTGAAGTATTAAT 600
Db 541 TATCTTGAAGATTTGGCTTACAGATTAATCAATCTTAAATCTTGAAGTATTAAT 600
QY 601 CAGTTCCAAAGCAGGGGAGAGAAATTCACATACTTTAGCAGGGTCAATTAACAACG 660
Db 601 CAGTTCCAAAGCAGGGGAGAGAAATTCACATACTTTAGCAGGGTCAATTAACAACG 660
QY 661 AAAGCTGAAATATTAATTTATGCTTACGATGTGCAAGCTGCAATGTCTATTTATTA 720
Db 661 AAAGCTGAAATATTAATTTATGCTTACGATGTGCAAGCTGCAATGTCTATTTATTA 720
QY 721 TTAAGGGAACCAAGTTAAATTAATAAAGAAATGGGAACTAGTGTGTCAACGTTGATCA 780
Db 721 TTAAGGGAACCAAGTTAAATTAATAAAGAAATGGGAACTAGTGTGTCAACGTTGATCA 780
QY 781 GGGTCAAGGGAACCTGATTTGTAACGAGCGGTTAAAGCGGAAATTAAGATTAATTAAT 840
Db 781 GGGTCAAGGGAACCTGATTTGTAACGAGCGGTTAAAGCGGAAATTAAGATTAATTAAT 840
QY 841 TATGTGTAGGGTGTGTATTAACAAGGTTAGATCAGATTAAGACAGCGGGTCAAGATGCT 900
Db 841 TATGTGTAGGGTGTGTATTAACAAGGTTAGATCAGATTAAGACAGCGGGTCAAGATGCT 900
QY 901 GAAGTTGTGTCAAAATTAATTAATTTGTAAGAAATGA CGTTGGCGGTATTTGGAATTT 960
Db 901 GAAGTTGTGTCAAAATTAATTAATTTGTAAGAAATGA CGTTGGCGGTATTTGGAATTT 960
QY 961 ATTGCTATATTTTCAACTTAATTTGTAAGAAATTAATTCATTAACAAGTGTATTAAT 1020
Db 961 ATTGCTATATTTTCAACTTAATTTGTAAGAAATTAATTCATTAACAAGTGTATTAAT 1020
QY 1021 ACTAGGGAATTTTATACAGATCCAGTGGATATTCAAGGGGAAATTTATGTTGGGAACG 1080
Db 1021 ACTAGGGAATTTTATACAGATCCAGTGGATATTCAAGGGGAAATTTATGTTGGGAACG 1080
QY 1081 TTTTATAGCTTTTAATTCGTAGAAACCAATGGAACA CGGGGACCTGGTTTATGTTACTTGG 1140
Db 1081 TTTTATAGCTTTTAATTCGTAGAAACCAATGGAACA CGGGGACCTGGTTTATGTTACTTGG 1140
QY 1141 CTTCAAGCTATTAAGTATTAATGATCAATTTATTAATTTCAAGCTGTGTTATCTTAATG 1200
Db 1141 CTTCAAGCTATTAAGTATTAATGATCAATTTATTAATTTCAAGCTGTGTTATCTTAATG 1200
QY 1201 TGGGGGGGAACTGCTCATTAATGAAGACTTCAACAAGGGAACGCTGCTTTTCAAGTATG 1260
Db 1201 TGGGGGGGAACTGCTCATTAATGAAGACTTCAACAAGGGAACGCTGCTTTTCAAGTATG 1260
QY 1261 TCTGGAACCTACGAGTAAATTAATCCAGTAAATTAATTTTGGCAATTAACGATATATTTAA 1320
Db 1261 TCTGGAACCTACGAGTAAATTAATCCAGTAAATTAATTTTGGCAATTAACGATATATTTAA 1320

QY 1321 ATTAATTTATAGTAGTATTAATGAATGCAACCGTTTGGGTATTTCAATCCACAGGCAAT 1380
Db 1321 ATTAATTTATAGTAGTATTAATGAATGCAACCGTTTGGGTATTTCAATCCACAGGCAAT 1380
QY 1381 CTTGTTTCAAGTACGAGAAATTTTTCGACAACTATTAATCTTCTGTATAGGTAAAC 1440
Db 1381 CTTGTTTCAAGTACGAGAAATTTTTCGACAACTATTAATCTTCTGTATAGGTAAAC 1440
QY 1441 AGTTCTGGGTACTCAGACAAATTAATCTGTGTTTACAGGTTATTAATTAAGATCTTACA 1500
Db 1441 AGTTCTGGGTACTCAGACAAATTAATCTGTGTTTACAGGTTATTAATTAAGATCTTACA 1500
QY 1501 CCTAGTCGTAACAAATTAATCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
Db 1501 CCTAGTCGTAACAAATTAATCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
QY 1561 TCCAGAGTTAAAGTATTTGGTTGACACATTAAGTAAAGTAAATTAATTAATTAATTAAT 1620
Db 1561 TCCAGAGTTAAAGTATTTGGTTGACACATTAAGTAAAGTAAATTAATTAATTAATTAAT 1620
QY 1621 CCAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
Db 1621 CCAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
QY 1681 TATGACAGAGTTAAGTACAGCTGAGGCTGTTTATTAACAGAGAGATTAATTAATTAAT 1740
Db 1681 TATGACAGAGTTAAGTACAGCTGAGGCTGTTTATTAACAGAGAGATTAATTAATTAAT 1740
QY 1741 CCTTATCAAGCAAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
Db 1741 CCTTATCAAGCAAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
QY 1801 GTTAACTTGGCTAGAGGAGTGAAGAGCTGTTTCCAGTGAAGAGTGAAGTGAAGTGAAG 1860
Db 1801 GTTAACTTGGCTAGAGGAGTGAAGAGCTGTTTCCAGTGAAGAGTGAAGTGAAGTGAAG 1860
QY 1861 AGTTCTGTTTCAAGTCAATTTTCTGCTGACAGCTGAGGCTATTAATTAATTAATTAAT 1920
Db 1861 AGTTCTGTTTCAAGTCAATTTTCTGCTGACAGCTGAGGCTATTAATTAATTAATTAAT 1920
QY 1921 TATGTGACACCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TATGTGACACCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
QY 1981 CTATCTGTTTACCACTTATTTGTTGACAAAGTGAATTTATCCAAATGACATCCAAAT 2040
Db 1981 CTATCTGTTTACCACTTATTTGTTGACAAAGTGAATTTATCCAAATGACATCCAAAT 2040
QY 2041 GAAAAATGTAAGAAATGCAATTCGAAAGGACATTAATTAATTAATTAATTAATTAATTA 2100
Db 2041 GAAAAATGTAAGAAATGCAATTCGAAAGGACATTAATTAATTAATTAATTAATTAATTA 2100
QY 2101 TTGGAACCAAAAAAGAGATTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 2145
Db 2101 TTGGAACCAAAAAAGAGATTTGTAATTAATTAATTAATTAATTAATTAATTAATTA 2145

RESULT 2
CO868325 2019 bp DNA linear PAT 13-SEP-2004
LOCUS CO868325
DEFINITION Sequence 26 from Patent WO2004074462.
ACCESSION CO868325
VERSION CO868325.1 GI:51998371
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi,N., Hargiss,T., Koziele,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 26 02-SEP-2004;

FEATURES
source

Athenix Corporation (US)

Location/Qualifiers

1..2019

/organism="Bacillus thuringiensis"

/mol_type="unassigned DNA"

/db_xref="taxon:1428"

CDS

1..2019

/note="unnamed protein product"

/codon_start=1

/transl_table=1

/protein_id="CAH3957.1"

/db_xref="GI:51998372"

/translation="MKKMSGYONTNEYEILIDGSPNNMNSRYPKADPNIPINLIDA
CDVSIIRKVEDSVSDVADFEGETATVODYILATLEMDLTKSPKCLADVVKP
QAREBDFTKLASLSQKAILLPYVQAAVHLLLDVAYKKEWELVCEPLVP
GSRDIDENRILKAKIKEYTNYCVGMKNGDIQROAGTSLEWSEKFKPREMTLAL
DIALPFTYDFEKYPLATSVELPSEIYTDPEVSGNGYMERFESFVSANGRFG
LMTLOALIDVSHINLOGLSGMGSTHEDPTKNGAFORMSGTSMNPNIIFG
NTDIFKISLARVAMPFVGYISIPRHVSAEFPFTTLNPLFVNSGYSOTIEVL
PGINKDLPSRINYSRHSNAACVONETSIVNFGVHTSMKDNRLYPDKITQIPAV
KAPLPAGTGYAGGYTAGGYTGADVTLTPYQASLKITLSAPTNKNYERLRYASG
GPPFPERVMSPSVSANFSPATGYSFDYVDLTVTTFNOSGVEIITQNSGYHL
IVDKVEPIPIDIEKTKCQFEGDICRGGVQSLKTKETVNSLFIN"

ORIGIN

Query Match 94.1%; Score 2019; DB 6; Length 2019;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 127 GTGAAAATATGAAATCTTATCAAAATCAAAATGAAATTCGATGCTCCCG 186
DB 1 GTGAAAATATGAAATCTTATCAAAATCAAAATGAAATTCGATGCTCCCG 60
QY 187 AATPACAAATATGTCAAACAGATATCTTTGCAAGAGATCCAAATATTTCTAT 246
DB 61 AATPACAAATATGTCAAACAGATATCTTTGCAAGAGATCCAAATATTTCTAT 120
QY 247 AACCTGACCGCTTGTCAAGGAGCCATGCGAAGATACGTGGGAATCATCTCGATATA 306
DB 121 AACCTGACCGCTTGTCAAGGAGCCATGCGAAGATACGTGGGAATCATCTCGATATA 180
QY 307 GTAATCTATGGAATCATCTTATPACATTTCTGTAAACCCGGTATAGGTGAATTCCT 366
DB 181 GTAATCTATGGAATCATCTTATPACATTTCTGTAAACCCGGTATAGGTGAATTCCT 240
QY 367 GTAATATTTTCAATATATAAACAATCATTCGGTCTTCTGTCAATCTGTGGCAGCACT 426
DB 241 GTAATATTTTCAATATATAAACAATCATTCGGTCTTCTGTCAATCTGTGGCAGCACT 300
QY 427 TCTATATGTAATTAATGATCTATTAATTCGTAAGAGGTAGACAGAGCGTGTAAAGTAC 486
DB 301 TCTATATGTAATTAATGATCTATTAATTCGTAAGAGGTAGACAGAGCGTGTAAAGTAC 360
QY 487 GGGGTTCAGATATTTGAGGTGAATGATCGCTTATCAAGATATATCTTCAATATCTT 546
DB 361 GGGGTTCAGATATTTGAGGTGAATGATCGCTTATCAAGATATATCTTCAATATCTT 420
QY 547 GAGGATTTGCTTACAGATAATCAAAATCTTAAAGGCTGATGCGATGTTAAACGTTCC 606
DB 421 GAGGATTTGCTTACAGATAATCAAAATCTTAAAGGCTGATGCGATGTTAAACGTTCC 480
QY 607 CAAGCAGGGAAGAAGATTTCACTAAAATTGAGCAGGCTCATTTATCAAGACAGAAAGCT 666
DB 481 CAAGCAGGGAAGAAGATTTCACTAAAATTGAGCAGGCTCATTTATCAAGACAGAAAGCT 540
QY 667 GAAATATTTATTTGCTTACAGATAATCAAAATCTTAAAGGCTGATGCGATGTTAAACGTT 726
DB 541 GAAATATTTATTTGCTTACAGATAATCAAAATCTTAAAGGCTGATGCGATGTTAAACGTT 600
QY 727 GAGCAGTTTAAATATAAAGAAATGAGGAGCTAGTGTGTCCACGTTGTATCCAGGATCA 786
DB 601 GAGCAGTTTAAATATAAAGAAATGAGGAGCTAGTGTGTCCACGTTGTATCCAGGATCA 660
```

```

QY 787 GGGAGAACTGATGTTGTAACGACCGGTTAAAGCCGAAATATAAAGCTATCTAATATTTCT 846
DB 661 GGGAGAACTGATGTTGTAACGACCGGTTAAAGCCGAAATATAAAGCTATCTAATATTTCT 720
QY 847 GTAAGGCTGATATAAAGGCTTTAGATCAATATAAGACAGGCGGGTACAAGTGTGGAAGTT 906
DB 721 GTAAGGCTGATATAAAGGCTTTAGATCAATATAAGACAGGCGGGTACAAGTGTGGAAGTT 780
QY 907 TGGTCGAAATTTATATAAATTTCTGAGAAATGACGTTGGCGGTAATGATATTTATTTCT 966
DB 781 TGGTCGAAATTTATATAAATTTCTGAGAAATGACGTTGGCGGTAATGATATTTATTTCT 840
QY 967 ATATTTTCAACTTATGATTTTGAAGAAATATCCATTAGCAACAAGTGTGATTAAGTAC 1026
DB 841 ATATTTTCAACTTATGATTTTGAAGAAATATCCATTAGCAACAAGTGTGATTAAGTAC 900
QY 1027 GAAATTTATACATACAGTGGGATATTCAGGGGGGAAATTAAGTTGGGAAACGTTTCTT 1086
DB 901 GAAATTTATACATACAGTGGGATATTCAGGGGGGAAATTAAGTTGGGAAACGTTTCTT 960
QY 1087 AGCTTTAATTCGGTATGAGCAATATGAAACACAGGGGACCTGTTAGTTACTTGGCTTCAA 1146
DB 961 AGCTTTAATTCGGTATGAGCAATATGAAACACAGGGGACCTGTTAGTTACTTGGCTTCAA 1020
QY 1147 GCTATAGATATATATATGATCTATCTATTAATCTTACGTTGTTATCTTATGAGCTGGGG 1206
DB 1021 GCTATAGATATATATATGATCTATCTATTAATCTTACGTTGTTATCTTATGAGCTGGGG 1080
QY 1207 GGAATCTGCAATATGAGACTTCAAGAGGATACGGTCTTTCAACCTATGCTCGCA 1266
DB 1081 GGAATCTGCAATATGAGACTTCAAGAGGATACGGTCTTTCAACCTATGCTCGCA 1140
QY 1267 ACTACAGATATATATCACTAATATTTTGGCAATACCGATATATTTAAATATTT 1326
DB 1141 ACTACAGATATATATCACTAATATTTTGGCAATACCGATATATTTAAATATTT 1200
QY 1327 TCAATAGCTATGATATGCAATGCAACCGTTGTTGGGATTCATATCCACGGCATCTTGT 1386
DB 1201 TCAATAGCTATGATATGCAATGCAACCGTTGTTGGGATTCATATCCACGGCATCTTGT 1260
QY 1387 TCAAGTGCAGAAATTTTTCGACAACTAAATCTTCTGATATAGGTAACAGTTCT 1446
DB 1261 TCAAGTGCAGAAATTTTTCGACAACTAAATCTTCTGATATAGGTAACAGTTCT 1320
QY 1447 GGGTACTCAGACAAATGATCTGTGTACAGATTAATTAAGATCTACCACTAGT 1506
DB 1321 GGGTACTCAGACAAATGATCTGTGTGTACAGATTAATTAAGATCTACCACTAGT 1380
QY 1507 CGTACAAATTAATCTGATATGATTAATCAAAATGCGGCAATGTGTCAAAATGAACCTCCAG 1566
DB 1381 CGTACAAATTAATCTGATATGATTAATCAAAATGCGGCAATGTGTCAAAATGAACCTCCAG 1440
QY 1567 GTTAAAGTATTTGGTTGGAACATATCAAGATTAAGAAATTAATGAATTTATCCAGAT 1626
DB 1441 GTTAAAGTATTTGGTTGGAACATATCAAGATTAAGAAATTAATGAATTTATCCAGAT 1500
QY 1627 AAAATTAACGCAATTTCTGCAATGAAAGCTTTTGGCCCTACAGACAGGATCAGGATATGCA 1686
DB 1501 AAAATTAACGCAATTTCTGCAATGAAAGCTTTTGGCCCTACAGACAGGATCAGGATATGCA 1560
QY 1687 GAGGTTACGTCACAGCTGGGCTGTGTTATACAGAGAGAGATGTATGAAACGTTATCTTAT 1746
DB 1561 GAGGTTACGTCACAGCTGGGCTGTGTTATACAGAGAGAGATGTATGAAACGTTATCTTAT 1620
QY 1747 CAAGCAAGTTTAAATATAAGTTTAACTTCTGCAACCAAGAAATTAATTAACGTTTAA 1806
DB 1621 CAAGCAAGTTTAAATATAAGTTTAACTTCTGCAACCAAGAAATTAATTAACGTTTAA 1680
QY 1807 CTTGCTAGCGAGATGAGGACCTGCTGCTTCCGATGAGAAAGATGTGCGCAAGTTCT 1866
DB 1681 CTTGCTAGCGAGATGAGGACCTGCTGCTTCCGATGAGAAAGATGTGCGCAAGTTCT 1740
```


QY	1336	AGATATGCAATGACACCGTTGTTGGATTCATCCAGCGCATCTTGTTCACGTGCA	1335
Db	1201	AGATATGCAATGACACCGTTGTTGGATTCATCCAGCGCATCTTGTTCACGTGCA	1260
QY	1396	GAATTTTTCGACACACATAAATCTTCTGTATGAGTAAACAGTTCTGGGATCTCA	1455
Db	1261	GAATTTTTCGACACACATAAATCTTCTGTATGAGTAAACAGTTCTGGGATCTCA	1320
QY	1456	CAGCAATGGAATCTGTATCCAGGATTTATATAGATCTACCACTAGTGTGTAAT	1515
Db	1321	CAGCAATGGAATCTGTATCCAGGATTTATATAGATCTACCACTAGTGTGTAAT	1380
QY	1516	TACCTCTAGATATCAAAATGCGGCATGTGTCAAAATGAAACCTCCAGATTAACTA	1575
Db	1381	TACCTCTAGATATCAAAATGCGGCATGTGTCAAAATGAAACCTCCAGATTAACTA	1440
QY	1576	TTTGGTTGACACATACAAAGTATGAAAAAGATATCGAATTTATCCAGTAAATTCG	1635
Db	1441	TTTGGTTGACACATACAAAGTATGAAAAAGATATCGAATTTATCCAGTAAATTCG	1500
QY	1636	CAAAATTCCTGACATGAAAGCTTTTCCCTACGACAGGATGACAGATATGACAGATTAC	1695
Db	1501	CAAAATTCCTGACATGAAAGCTTTTCCCTACGACAGGATGACAGATATGACAGATTAC	1560
QY	1696	GTCAAGCTGGGCTGTTATACAGAGAGATGATGATTAAGTTAACTTATCCAGCAAGT	1755
Db	1561	GTCAAGCTGGGCTGTTATACAGAGAGATGATGATTAAGTTAACTTATCCAGCAAGT	1620
QY	1756	TTAAATATACGTTTAACTTTGACACCAACGAATTAATTCACGTTGATGACCTTGCTAC	1815
Db	1621	TTAAATATACGTTTAACTTTGACACCAACGAATTAATTCACGTTGATGACCTTGCTAC	1680
QY	1816	GCGAGTGAAGGACCTGCTCCGCTCCGATGAGTAAAGATGTCGCCAAGTCTGTTCAAT	1875
Db	1681	GCGAGTGAAGGACCTGCTCCGCTCCGATGAGTAAAGATGTCGCCAAGTCTGTTCAAT	1740
QY	1876	GCTAATTTTCTGCTCCAGCTACAGGTCGCTATAGTTGATTTATGTCGACACCTTA	1935
Db	1741	GCTAATTTTCTGCTCCAGCTACAGGTCGCTATAGTTGATTTATGTCGACACCTTA	1800
QY	1936	GTTACTACATTTATCAATCAGTGTGTAATTAATTAACAATTCATCTGTTTACAC	1995
Db	1801	GTTACTACATTTATCAATCAGTGTGTAATTAATTAACAATTCATCTGTTTACAC	1860
QY	1996	CTTATTTGTGACAAAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACGAA	2055
Db	1861	CTTATTTGTGACAAAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACGAA	1920
QY	2056	TGTTAATTTCCAGAGACATTTGATGATGTGAGAGATCAATCTTGAAAAACAAAAA	2115
Db	1921	TGTTAATTTCCAGAGACATTTGATGATGTGAGAGATCAATCTTGAAAAACAAAAA	1980
QY	2116	GAGATTGTAATAGTTTATTTATCAATTA 2145	
Db	1981	GAGATTGTAATAGTTTATTTATCAATTA 2010	

RESULT 4
AB074414 3746 bp DNA linear BCT 14-JUN-2003
LOCUS
DEFINITION
Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40orf2 protein, partial and complete cds.
ACCESSION
AB074414
VERSION
AB074414.1 GI:16945771
KEYWORDS
SOURCE
Bacillus thuringiensis serovar aizawai
ORGANISM
Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
AUTHORS
TITLE
1 Ito, T., Sahara, K., Asano, S. and Bando, H.
Cloning and Expression of Novel Crystal Protein Genes from Bacillus

QY	1336	AGATATGCAATGACACCGTTGTTGGATTCATCCAGCGCATCTTGTTCACGTGCA	1335
Db	1201	AGATATGCAATGACACCGTTGTTGGATTCATCCAGCGCATCTTGTTCACGTGCA	1260
QY	1396	GAATTTTTCGACACACATAAATCTTCTGTATGAGTAAACAGTTCTGGGATCTCA	1455
Db	1261	GAATTTTTCGACACACATAAATCTTCTGTATGAGTAAACAGTTCTGGGATCTCA	1320
QY	1456	CAGCAATGGAATCTGTATCCAGGATTTATATAGATCTACCACTAGTGTGTAAT	1515
Db	1321	CAGCAATGGAATCTGTATCCAGGATTTATATAGATCTACCACTAGTGTGTAAT	1380
QY	1516	TACCTCTAGATATCAAAATGCGGCATGTGTCAAAATGAAACCTCCAGATTAACTA	1575
Db	1381	TACCTCTAGATATCAAAATGCGGCATGTGTCAAAATGAAACCTCCAGATTAACTA	1440
QY	1576	TTTGGTTGACACATACAAAGTATGAAAAAGATATCGAATTTATCCAGTAAATTCG	1635
Db	1441	TTTGGTTGACACATACAAAGTATGAAAAAGATATCGAATTTATCCAGTAAATTCG	1500
QY	1636	CAAAATTCCTGACATGAAAGCTTTTCCCTACGACAGGATGACAGATATGACAGATTAC	1695
Db	1501	CAAAATTCCTGACATGAAAGCTTTTCCCTACGACAGGATGACAGATATGACAGATTAC	1560
QY	1696	GTCAAGCTGGGCTGTTATACAGAGAGATGATGATTAAGTTAACTTATCCAGCAAGT	1755
Db	1561	GTCAAGCTGGGCTGTTATACAGAGAGATGATGATTAAGTTAACTTATCCAGCAAGT	1620
QY	1756	TTAAATATACGTTTAACTTTGACACCAACGAATTAATTCACGTTGATGACCTTGCTAC	1815
Db	1621	TTAAATATACGTTTAACTTTGACACCAACGAATTAATTCACGTTGATGACCTTGCTAC	1680
QY	1816	GCGAGTGAAGGACCTGCTCCGCTCCGATGAGTAAAGATGTCGCCAAGTCTGTTCAAT	1875
Db	1681	GCGAGTGAAGGACCTGCTCCGCTCCGATGAGTAAAGATGTCGCCAAGTCTGTTCAAT	1740
QY	1876	GCTAATTTTCTGCTCCAGCTACAGGTCGCTATAGTTGATTTATGTCGACACCTTA	1935
Db	1741	GCTAATTTTCTGCTCCAGCTACAGGTCGCTATAGTTGATTTATGTCGACACCTTA	1800
QY	1936	GTTACTACATTTATCAATCAGTGTGTAATTAATTAACAATTCATCTGTTTACAC	1995
Db	1801	GTTACTACATTTATCAATCAGTGTGTAATTAATTAACAATTCATCTGTTTACAC	1860
QY	1996	CTTATTTGTGACAAAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACGAA	2055
Db	1861	CTTATTTGTGACAAAGTGAATTTATCCCAATTGACATCCAAATTTGAAAAATGACGAA	1920
QY	2056	TGTTAATTTCCAGAGACATTTGATGATGTGAGAGATCAATCTTGAAAAACAAAAA	2115
Db	1921	TGTTAATTTCCAGAGACATTTGATGATGTGAGAGATCAATCTTGAAAAACAAAAA	1980
QY	2116	GAGATTGTAATAGTTTATTTATCAATTA 2145	
Db	1981	GAGATTGTAATAGTTTATTTATCAATTA 2010	

thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins
Unpublished
2 (bases 1 to 3746)
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (14-NOV-2001) Takekoshi Ito, Graduate school of Agriculture, Hokkaido University, Kita-9Jyuu Nishi-9chome, Kita-Ku, Sapporo-shi, Hokkaido 060-8589, Japan
(E-mail: ito-t@ags.agr.hokudai.ac.jp, Tel:81-011-716-2487)
location/Qualifiers
1. 3746
/organism="Bacillus thuringiensis serovar aizawai"
/mol_type="genomic DNA"
/serovar="aizawai"
/isolate="Bun1-14"
/db_xref="taxon:1433"
1. 2002
/gene="cry40A"
1. 2002
/gene="cry40A"
/codon_start=2
/transl_table=2
/product="putative mosquitocidal toxin"
/protein_id="BA072018.1"
/db_xref="GI:16945772"
/translation="NSYENKREVEILSSNNNTMPNRYPPANDRMTSMFNDQGI
SMDIWESEATLISIGIDLIEFLMEPELAGINTLFSILGKLIPTNHOSVSLISIDLI
SIRKEVADSVLSDAICRPLDGKLNKREYVLPLEMLDGLKPLQNTSDNLSIDLVK
YPLSESDNEIIGSLARNAOILIPYCAKCOLILRDAVOVEBOWPPLSAE
MNSSELSPNSGDFPDYERLCKRIAPLTDYCYEYQAGLNDIKQAGTADTMAK
NKRREMLTVLDLIALFQYDFKRYPLPVELTRRIYDYPVSGTGYSMRWYTG
AFNTEANGRGRLVTWMLRSIGYNEVSRYSGWGTGTHYEDYTGNGNFORSGT
TSNDLRISPPNSDIFKIESKALINLVGINAPREYSALESSTAFILYDAGNS
GLSMTSTSLPGIKNPEPSRYDYSHLNMAACVAGANSRLINVTGWTHTSKYNLIY
PDITTOIYPAKADISPTGCGVYAGSGHCGANVSLPYRSRLKRLIPASTNRYLY
RVRTSTSNRLVERSPSSINSYFPLSTGDSFGYVDLITVFNFQVEIITIQ
NLDTPIVNDVRELPVNSTALEYKSLERKADVDVNDLVRK"
2070. 3746
/gene="40orf2"
2070. 3746
/gene="40orf2"
/codon_start=1
/transl_table=1
/product="Cry40orf2 protein"
/protein_id="BA072019.1"
/db_xref="GI:16945773"
/translation="MTNNGKNTLKTETTDYEIDQAAISIECMSDEHSPEKXWMLNE
VKAKLISGRNLONQDPDPIGNDRKFFGNITIGSNSTFKGNFLQSGARDYGT
IFPLTYIQKIDESKLRPYTRYRVRGFVSSKDLRLWTRYGKETIDAMNVPNDLIYQ
PNPSGDSRCSSESOYVQYPPPTDGYADRYACPSSDKRYMCHDRHPDFDIPT
GELDTYNTVIGIDVLFKISNPDGATLGNLEIEGPIGTALTRVQKKEKKQDMRK
KRWETQOAVDPKAOVDLTFLTNBOELHLYLTDYIOTLIDMYSFPFITYMTGYDAG
MNYDVGQNLARIYMOAVNLYDARNVLTNGSPKTYQCMHAGRAAOVQIDGASVLYS
MNSAGVSONLHADDSHYMLRYLAKKRPKGYVTMDCNGOETLFGSCBETMTRK
TVVFPESDVRRIEIGETGTFYVDSIELCMQGYASNNPNPGLNMTGOSYNGVNYON
TSDVYHOGYTNNTNONSNNMYNQNTHNDLHSGCTCNQGNISGCTCSOG"

ORIGIN
Query Match 44.3%; Score 949.2; DB 1; Length 3746;
Best Local Similarity 71.4%; Pred. No. 7.2e-167;
Matches 146; Conservative 0; Mismatches 498; Indels 88; Gaps 13;
QY 138 GAATTCCTATCAAAATCAATGAAATGGAATTTCTGATGTTCCCGGATAACACAAA 197
Db 1 GAATTCATATGAAATATGAAATGATGAAATATGGAATCTTCAATGAAATACACAAA 60
QY 198 TATGTCAAAGATATCTTTTGGCAAGATCCAAATATATTTCTATTTAACTGGAGCC 257
Db 61 TATGTCAAAGATATCTTTTGGCAAGATCCAAATATATGATCTATGCTTTTCAATGTA 120
QY 258 TTGTGAGGAAGGCAATGCAAGATACGTGGGAATCGTCCGATTTAGTAATATTTGG 317
Db 121 TTGTGAGGAATCTCATGGATGAAATTTGGGAATACGCCGAACGATTAACAGTATGG 180

QY 318 GACATACCTTATCAATCTTGGCTAGAACCGGTAATAGTGAATTCCTGTAAATTTTC 377
DB 181 GATAGATCTTATAGAGTTTGTGATGAACTTATGGGTGATTAATACATTTTTC 240
QY 378 AATTAATTAACAACTCATTCCTGCTTCTGTCAATCTGTGACAGCACTTTCTATATGTA 437
DB 241 AATTAATAGAAAATCAATTCGCACTAATCATCATCTGTGTCAAGCACTTTCTATATGTA 300
QY 438 TTATAGATCTAATTTCTGTAAAGGTGAGAGAGGTGTATAGTACGGGTT--GC 494
DB 301 TTTATATCTAATATTCGTAAAGGTGAGCGATGATGTTTAAAGTATCGAATTTGACG 360
QY 495 AGATTTTGAGGTGAAATGACTGCTTATCAAGATTTATCTTCAATCTTGAGATG 554
DB 361 ATTTTGGAGGTAAATGAAAAATTAAGAGTATTAATCTTCTTATCTTGAGGCTTG 420
QY 555 GCTTACG-----ATTAATCAAAATCCTTAAAAAATTTGCTGACGTAGTTAA 599
DB 421 GCTTAAAGACGTAACCACTTCAAAAGCAAAATTAATTTGTATGCGAATAATGTTAA 480
QY 600 ACAGTTCCAGACACGGGAAGATTTCTAATACTTTTACAGGCTCATTAACAACA 659
DB 481 ATATTTGAACTTTCAGAAAAGGATTTTAATGAATTTCTAGAGAGATCATTTAGCAAGAAA 540
QY 660 GAAAGCTGAATATTTATTTATGCTC-TACGTATGTGCAAGCTGCAATGTGCATTTATAC 718
DB 541 CAATGCTCAAAATTTGTATTACCTTACTTTTGGCAAGCTGCAAAATGT-CAATTAATAT 599
QY 719 TATTTAAGGACGAGTTAAATTAATTAAGAAATGGGACATAGTGTGCCACCGTTATAC 778
DB 600 TATTTAAGGATGAGTCAATATAGAGAACATATGTTCCATTTTGAAGTGCAGAGATG 659
QY 779 CAGGTCAGGGAGAAC-----TGATTTGTAACGAC 808
DB 660 TAAGATCGGAATTAATATCACTTAACAGTGTGTGATTTTACCGGATTTACTATGACG 719
QY 809 GGTAAAAAGCAAAATTAAGAGTACTAATTAATTTGTAGGGTGTATTAACAAGGTT 868
DB 720 GATTTAAATGTAAATATGACAGATATACGATTAATGTGAATATGTTATCAAGCGGTT 779
QY 869 TAGATCAGATTAACAGCGCGGTGCAAGTCTGAAGTTGTGCGAAAATTTAATTAATTTTC 928
DB 780 TAATCAATTAATAAACAGCGCGGTGCAAGTCTGCACTGCGCAAAATTTAATTAATTTTC 839
QY 929 GTAGAGAAATGAGTGTGGGTATGTAATTAATTTGTATATTTTCCAACTTAATGATTTTG 988
DB 840 GTAGAGAAATGAGTGTGACGTATGATTAATTTGCTATATTTCAAACTTAATGATTTTCA 899
QY 989 AAAAAATTCATTAGCAACAAGGTAGATTAATACTAGGAAATTTATACAGATCCAGTGG 1048
DB 900 AGAAATATCCATCAACAACATGTAGAGTTAACTAGGAAATTTATACAGATCCAGTGG 959
QY 1049 GATATTCAGGGGGAATTAATGTTGGAGCGGTTTTTAC-----TTTAATTCGGTAG 1102
DB 960 GATATTCATCAGAACTTATAGCTGTTAAAGTATGACCGGTGCTTTAATAACGTTAG 1019
QY 1103 AAGCAATGGAACACGGGGACCTGGTTTAACTTCTTGGCTTCAAGCTATAGATATATA 1162
DB 1020 AAGCTATAGGAACACGGGGACCTGGCTTATGTTAGCTTGAAGATATAGATATATA 1079
QY 1163 GTCAATCTAATTAATCTTCAAGCTTGTATCTATGAGTGGGGGAACTCGTATATAG 1222
DB 1080 ATAGATATGTT-----TCGAGATATTTTACCGGCTGGTAGAGAACTCGGATATAG 1130
QY 1223 AAGACTTACAAAAGGTGACGGTGTCTTTTCAACGTATGTCTGAACTACAGATATATATC 1282
DB 1131 AAGACTTACAAAAGGTGACGGTGTATTTTCAACGTATGTCTGAACTACAGATATATATC 1190
QY 1283 CAGGTATATTTATTTTGGCAATACGATATATTTAATTTATTTCACTTGAAGATATAG 1342
DB 1191 TAGGTATATTTAGTTTTCAAAATTCGATATATTTAATAATGTAATCAAAAGCTA---TCA 1247

QY 1343 CAATGCAACCGTTTGGGTATTCATCCACGCGCATCTGTGTTTCAGCTGAGAAATTTT 1402
DB 1248 TGAACTTACTAGAGAGATTTAAACCTAGACCGAGATATGTGTTTCACTGCAAGATTTTA 1307
QY 1403 TTCGACAACTAAATTAATCTTCTGTATGAGGTAAACAGTTCTGGTA---CTACAGA 1459
DB 1308 GTGAGTCAACAGCATTTATATACCTGTATGATGACAGTAAATAGTGGCTAACAGCATGA 1367
QY 1460 CAATGAATCTGTGTTACAGAGTAATTAATAAGATCTACACCTAGCTGTAATTAATCT 1519
DB 1368 CAATTAATCTAAGTTAATACAGGATTAATAGA---ATCCAAACCTAGTTAAGATTAATCT 1424
QY 1520 CTCATAGATTTATCAATGCGGACATGTGTTCAAAATGAAACCTCAGAGTTAAAGTATTG 1579
DB 1425 CTCATAGATTTATCAATGCGGACATGTGTTGAGCTGCGCAACAGCAATTAAGTATATG 1484
QY 1580 GTTGGACACATCAAGTATGAAAAAAGATATCGAATTTATCCAGTAAATTTACGCAAA 1639
DB 1485 GTTGGACACATCAAGTATGCAAAATATATCTAATTTATCCAGCAAAATTTACACAAA 1544
QY 1640 TTCCTGACATTAAGCTTTTGGCCCTACAGCAGGTACAGGATATGAGAGGTTAGTGA 1699
DB 1545 TACCGGCGGTGAAAGCTTTGTATATATCGAATCA-----GGCGCAGGCTCAAGTCA 1595
QY 1700 CAGCTGGGCTGGTTATACAGAGAGATGTAGTAACTTACCTTATCAAGCAAGTTTAA 1759
DB 1596 TAGCTGACCTGGTCTATACAGAGAGAAATGTATAGCTTATCCATTTATTTACCGTTTAA 1655
QY 1760 AATTAAGTTTAACTTCTGCAACCCAGATPAAAAATTTACCGTGTAGACTTCCGTACGCA 1819
DB 1656 AATTAAGTTTAACTTCTGCAACCCAGATPAAAAATTTACCGTGTGTAGAGTTCGTATACAA 1715
QY 1820 GTGAGAGACCTGGTCCGTCCAGTATGAAAGATGTGCGCAAGTCTGTGTTCAAAAGCTA 1879
DB 1716 GTACGAGCAATGTATGATTTATGAAAGATGTGCGCAAGTCTGTATTAATTAATGTT 1775
QY 1880 ATTTTCTGCTCAGCTACAGGTGCTATAGTTCATTTATTAATGAGACACCTTAGTTA 1939
DB 1776 ATTTTCTTCTCATCTACAGGCTCGTGATTTCAATTTGGCTATGAGACACCTTAGTTA 1835
QY 1940 CTACATTTAATCAATCAGGTGTTGAAATTAATTAACAAAATCTATCTGTTAACACCTTA 1999
DB 1836 CTACATTTAATCAACAGGTGTTGAAATTAATTAACAAAATCT---TGATATCCCTAATTA 1892
QY 2000 TTGTGACAAAGCGAATTTATCCCAATTGA---CATCCAAATGGAATAATGACGAATG 2057
DB 1893 AGCTTGACAAAGTTGAATTTATCCAGTCAATTTTACGCGCTTAGAATATGAAAGAAAC 1952
QY 2058 TCATATCGAAGAGACATATGTATGATGTGAAGAGTACATCTTGGAACAAAAGAA 2117
DB 1953 AAAGTCTAGAAAAGGCAACAAGATGTATGTAATTTATTTGTTAAGTAAATTAAGTAT 2012
QY 2118 GATTGTAATAG 2129
DB 2013 GTACGAAAGTAG 2024

RESULT 5
Q0868311
LOCUS CQ868311 5980 bp DNA linear PAT 14-SEP-2004
DEFINITION Sequence 12 from Patent WO2004074462.
ACCESSION CQ868311
VERSION CQ868311.1 GI:51998357
KEYWORDS
SOURCE
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
1 Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
AUTHORS Delta-endotoxin genes and methods for their use
TITLE Patent: WO 2004074462-A 12 02-SEP-2004;
JOURNAL Athenix Corporation (US)

AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Cloning and Expression of Novel Crystal Protein Genes from *Bacillus*
thuringiensis subsp. *aizawai* Encoding Mosquitocidal Proteins
JOURNAL Unpublished
AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2003) Takeshi Ito, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience,
Kita-9jo, Nishi-8chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan
(E-mail: ito-t@obs.agr.hokudai.ac.jp, Tel: 81-11-706-2487 (ex.2487))
FEATURES
source
1. .4100
/organism="Bacillus thuringiensis serovar aizawai"
/mol_type="genomic DNA"
/strain="Bun1-14"
/serovar="aizawai"
/db_xref="taxon:1433"
267. .273
/note="putative"
279. .2279
/gene="cry40-1 like"
279. .2279
/codon_start=1
/transl_table=1
/product="putative mosquitocidal toxin"
/db_xref="GI:31745044"
/translation="MNSYQNKNEYELKSSPNNTNPNRYPFANDRMSPMWNCQGS
SPWNVESVASTGIGDILITFGEPSITGILNLPFVIGKLPSQONVASYICDL
SIRKEVDSVSDAGDENGVNNTQYVLTSLKKMLDAGEKTTGQLLDYTKHEF
SESEFALLKGSLSRPRGEITLLPTTQGANLHLRLDPVOYKAYMEKELENTRES
ELISPEDEGHRKBLAEHINCLITMQAGNQLQESGTSTNMLKPKFRTRENTLS
VLDIATFTYDENYKSTHIELSREVTIDPVINGMEQNLNGFTNLEAGTRSG
LVTMLKIDITFDEVTRYSGSPVAILRGAGTRHVEIYTGSSNTQRLSGTSSNVS
NIDFINSRLEIITSLARYALAGAAGNPGSPRYRVRVERSTGRYTLPEVNSPIS
SMTESEKLPGVNATGETFVFNRLSNACVQFQTSRNVGMTHIISMGANGVYYPKI
TOIPAYKAMEIRGTSVAGPGHTGNLVMSHVSYSIKFTCOOLKRYRVRVARD
GNCOIAMBRRGPGVVOEARHTVORTFSGSMYDSFKLIDITPMABDYTDLTIDL
ESGGALYIDKIEFI PDDLTTLEYEERNLEKTNVANDLFTN"
2348. .3949
/note="ORF2"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="BAC7649.1"
/db_xref="GI:31745045"
/translation="MFTSGAKNTLKIETTDYEDIDOAISIECMSDEHSPEKMWLMD
VKRAKLISGRNLONGDFEDFSGNDMTFENDIIGSNNSIFPKGNFLOMRGADIDYT
LFTVYVYOKIDESKLKPYRVRVGRVGSKNLKLWTRGKEIDAIIMVPPNDLSYMO
PSPSCGDYRCSSSRVNOGYPTPDGYADMTACPSNSEKRYKCHDRPHFDIT
GBLDITNVGIDVLEFKISNPDGYATIGNLVIESEGPLTEALTHVQKEKMKQHEK
KRMEYQYTNPAQAVDTLFTNEQELHYHTLTDHIONARLVOSIPIYIHDMLPDAPG
NMNDGYQGNLARIMQAVNYDARNVITNGDFTGLOGMHAGNAVOQIDGASVLT
NMAGVSONLHAQDHGYMLRYAKKEGPKGVVIMDCNGAETLKFSTCEBSGYTS
TYVPEPSDRVRIEIGETGETFYVDISIELCMGVASNNPHNGSNMYGOSYNNTYHN
DMLHSGCTCNQNSGCTCNGYNR"
ORIGIN
Query Match 37.9%; Score 812.4; DB 1; Length 4100;
Best Local Similarity 67.2%; Pred. No. 2.2e-141;
Matches 1358; Conservative 0; Mismatches 511; Indels 93; Gaps 11;
QY 115 ACTATATAGGAGTGAATAATGTAATCTTATCAAAATACAAATGAAATGAAATTCG 174
DB 258 ACTATACGAGAGTGAATGATGTAATCTATCAAAATGAAATGAAATGAAATTCG 317
QY 175 GATGTTCCCGGAATACAAATATGTCGAACAGATATCTTTTGGAAAGATCCAAAT 234
DB 318 AATCTTCACGGAATACAAATATACAAACAGATATCTTTTGGAAATGATCCGGAAT 377
QY 235 ATATTTCTATTAACCTGACGCTTGTCAAGGAAGCCATGCAAGATACGTGGGAATCA 294

DB 378 ATGTCTCCATGTCCTTGGAAATGATGTGCAAGGAACCCATGGAAGATGTGGGAATCA 437
QY 295 GTCTGGATATATGTAATCTTATGGGACATACCTTATTAACAATTTTGTCTAGAACCCGGTAT 354
DB 438 ACCCGAGATTCACAGGATATGGGATAGATCTTATTAACCTTTCTTGGAGAACCTTGCAATA 497
QY 355 GGGGAATTCCTGTAATATTTTCATPAATPAACAAATCATTCGGTCTTCTGGTCAATCT 414
DB 498 ACTGGATCAATTTTACTTTTTCAGATATAGGAACCACTACTTCCTTCTGGTCAAAAT 554
QY 415 GTGGACAGCACTTCTATATGATGATTTAGTATCTATATTTCTGTAAGAGGTAGACAGAGC 474
DB 555 GTGGATACATCTTCTATATGATGATTTATCTATATATTCGTAAGAGGTAGACAGAGT 614
QY 475 GTGTTAAGTGAAGCGGCTTGCACAAATTTTGAAGGTGAATGACGCTTATCAAGATTAAT 534
DB 615 GTTTTAAAGTGAAGCGCTATGAGATTTTAAATGTGTAGTGAATTAATTAACCAATATTAAT 674
QY 535 CTTCATTAATCTGAGGATTTGGCTTAAG-----ATTAATCAAAATCTTAAATAAATCTTGTCT 588
DB 675 CTTACTCTCTTAAAGATGGCTTATGATGAGGAAACCAACTACTGTCTCACTTACG 734
QY 589 GACGTATGTTAAACGTTCCAGACACGGAAGAGATTTCACTAACTTTAGCAGGGTCA 648
DB 735 GATGTAACTAAACATTTGCAATTTTCAAGAAAGGAGTTCAATGCACTTCAAAAGGCTCA 794
QY 649 TTATCAAGACAGAAAGCTGAATAATATTTATTTGCTTACGTATGTCAGACTGCCAAATGCG 708
DB 795 TTATCAAGACAGAAAGGTTAAATATTTGTTTATTTTAACTTAAACCAAGTGCAAATTTTG 854
QY 709 CATTATTAATCTTAAAGGACGCACTTAAATATTAATAAAGAAATGGGAGCTAGTGTGTCA 768
DB 855 CATTATTAATCTTAAAGGATTTTGGTTCAATTAAGCAATGTGGAAATAAGATTTGGCT 914
QY 769 CCGTGTATCAAGGTCAGGAGAA-----CTGATTTGTAACAGCGGTTAA 816
DB 915 ACAGAAATATGTGAATCGGAATGTGATACACTCTTTTGAATTAAGAGGCAATTTCA 974
QY 817 GCGAAATATTAAGATATCTAATTAATGTGAGGTGTATTAACAAGGTTTAATCG 876
DB 975 GAACAACATGACAGATATTAATCACTGTATTAACCTTGTATCAAGCGGTTTAATCA 1034
QY 877 ATTAAGACAGCGGATTAACAGTCTGAAGTTTGTGGAATTTAATTAATTTGTAGAGA 936
DB 1035 ATTAAGAGTCCGGTACAGATCTGAATAATGTTGAATTTAATTAATTTCCGAAGAGA 1094
QY 937 ATGACGTTGGCGGTATTTGATATTAATTTGCTATATTTCCAACTTATGATTTGAAAATAT 996
DB 1095 ATGACGTTGGCGGTATTTGATATTAATTTGCTATATTTCCAACTTATGATTTGAAAATAT 1154
QY 997 CCAATTGCAACAAGGTAGAGTTAACTAGGAAATTTATACAGATCCAGTGGATATTTCA 1056
DB 1155 AATATGAAACACATATTAAGTTATCTAGGGAAGTTTATACAGATCCAGTGGATATTAAT 1214
QY 1057 GGGGGAATTAATGTTGGGACGTTTTTTTACCTTTAATTCGGTGAAGCAATGGAGACA 1116
DB 1215 GG-----TTGGAAACAAATCTTACCAATGTTTTTAATACCTTAGAACCAATGGAGACA 1268
QY 1117 CGGGACCTGTTTATGTAATCTTGGCTCAAGCTATAGATATATATGATTTCTATTAAT 1176
DB 1269 CGGGACCTGTTTATGTTATCTTGGCTTAAGAGATATAGATATTTATCTAGTGAAGTACA 1328
QY 1177 CT-----TCAGCTTGTTATCTTAATGCTGGGGGGAATCTGTCTATAT 1221
DB 1329 GAGTATTCGGGGTGTCTCTGTGCTATCTTAAAGGCTGGGCGAGGCACTGTCTATAT 1388
QY 1222 GAAGACTTACAAAGGTTAAGGCTTTCACAGATATCTGGAACCTAGAGATATAT 1281
DB 1389 GAATTTATACAGGAGTTCATATCTTTGCAACGATATCTGGAACCTAGAGATATAT 1448
QY 1282 CCAAGTAATATATTTTGGCAATACCGATATATTTAAATTTTCACTAGATAT 1341

[illegible]

RESULT	8
CQ868314	
LOCUS	CQ868314
DEFINITION	Sequence 15 from Patent WO2004074462.
ACCESSION	CQ868314
	2073 bp DNA linear PAT 13-SEP-2004

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
COQ68314.1	GI:51998360	Bacillus thuringiensis Bacillus thuringiensis Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B. Delta-emotoxin genes and methods for their use Patent: WO 2004/074462-A 15 02-SEP-2004; Athenix Corporation (US) Location/Qualifiers	1. .2073 /organism="Bacillus thuringiensis" /mol_type="unassigned DNA" /db_xref="taxon:1428" 1. .2073 /note="unnamed protein product" /codon_start=1 /transl_table=1 /protein_id="CAH33952.1" /db_xref="GI:51998361" /translation="MSPYQKNKEVYELISSNNNTNPRIYPFANNRDMSTWISVNDCCG ISMDIEWSEVETITSGINLIEPIVIBSLGIGITLISIGKLIPTRQYTSALSI CDL LSIRKEVADSVLSADIADEQDLKNRYEYLSYLGAMLDKGRPLQKTNSNDIGOLVY YPLKISEDFENILIGGSLSRNNAOVLILPTFAOANOLILRLRAVOYKAAQMPPLSE MVSELSIPNSGCDPTGQDYERELKCTKAEVTNYCIWYQVGLNIOGGGCAPTWSE MKRRRETLTAVLDIALIPFYDEKPIPLPHVELITREITYDVAQVIGSGTYSWLRNEN TFNGLKNGTRGPELVWLSKIGIYNEYSRFAQWGVGNYHEDYITKGNOI FORMSGT TSDMLRINIDFQNDVYKITSIAIMNLVGETTARPEYKRSKADPRVGGPLNDAGNN GLSMRTIESTFPLVLSHNGVGRGSHRSNACVVGSRVNVGWTSTSKRNLIEA NOIIOIPAVKSYLYONLANAAYTVIGTGGTGLRFLFKTSEYNAVAVGGGRIILI NNTAGGOSYRIFRPAADAKAFPSVYIYPCGAGSNRPVLSKESYSGNYDLKSIDPEF AEITTPLEPSNIQDMVQANSPQSDVNVYLDKIEFLPSNTITLLEIEGRDLKTON AVNDLFTN"				

Query Match	34.5%;	Score 739.8;	DB 6;	Length 2073;
Best Local Similarity	69.7%;	Pred. No. 8.9e-128;		
Matches 1135;	Conservative 0;	Mismatches 422;	Indels 72;	Gaps 7;
QY	136	ATGAATCTTATCAAAATACAAATGATATGAAATTCCTGAGTGGTCCCGAATPAACA	195	
DB	1	ATGAGTCATATCAAAATPAATAATGATATGAAATATGAAATCTCATGGAATPAACA	60	
QY	196	AATATGTCAACACAGATATCTTTTGCAAAGATCCAAATATATTCCTATTAACCTGGAC	255	
DB	61	AATACGCCAAACAGATATCTTTTGCAAATPAATCGGATATATGCTACTATATCTTGGAAAT	120	
QY	256	GCTTGTCAAGGAGAGCCATGGCAGATACGTGGGAATCACTCTGGATATATGTAATTAAT	315	
DB	121	GATGTGAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAACGATPAACAAATTAAT	180	
QY	316	GGGACATACCTTATACAAATTCCTGCTGAACCCGGATAGGTGGGAATTCCTGTAAATATTT	375	
DB	181	GGGATAAATCTTATAGAGTTGTGATAGAACCTATGTTTGGTGGAAATTAATACCTATTA	240	
QY	376	TCATTAATTAACAAATCATTCCTGCTTCTGGATCAATCTGTGGAGACATTTCTATATGT	435	
DB	241	TCATTAATTAAGAAAACCTAATTCGACATTAATCTGTAACTGTGTACGACATTTCTATATGT	300	
QY	436	GATTAGTATCTAATATTCGTAAAGAGATGACGAGAGCGTGTAAAGTGAACGGGGTTGCA	495	
DB	301	GATTTATATCTAATATTCGTAAAGAGATGACGATATGTTTAAATGATGCGATTTGCA	360	
QY	496	GATTTTGAAGGTGAATGACTGCTTATCAAGATTATTAATCTTCATTAATCTTGAGATTGG	555	
DB	361	GATTTTGAAGGTGAATGAAAAATTAATAGAGATTAATCTTCTTATCTTGGGGCTTGG	420	
QY	556	CTTACAG-----AATTAATCAAAATCTGAAAAAATCTTGCGACGATAGTTAAA	600	
DB	421	CTTAAAGACGGTAACCACTTCAAAAGACAAATTAATCTGATATATCGGACATATTAATTAAT	480	

QY 601 CAGTCCAGCAGCGGAGAGATTGCTAACTTTAGAGGGGTCAATTCAAGCAG 660
 DB 481 TATTTTAACTTTAGAGAGAGATTGCTAACTTTAGAGGGGTCAATTCAAGCAG 540
 QY 661 AAAGCTGAAATATATATATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 541 AATGCTCAAGATATGTTATATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 721 TTAAGGAG 780
 DB 601 TTAAGGAG 660
 QY 781 GGGTCAG 840
 DB 661 AGATCGAATTAATATCACTTAACAGTGTGATTTTACCGGTGATTAAGAGAGAG 720
 QY 811 TTAAGGAG 870
 DB 721 TTAAGGAG 780
 QY 871 GATGAGATGAG 930
 DB 781 AATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
 QY 931 AG 990
 DB 841 AG 900
 QY 991 AAATATCATTAAG 1050
 DB 901 AAATATCATTAAG 960
 QY 1051 TATTCAG 1104
 DB 961 TATTCAG 1020
 QY 1105 GCAATGAG 1164
 DB 1021 GCAATGAG 1080
 QY 1165 CATTCTATTAATCTTACGTTGTTATCTTATGAGAGAGAGAGAGAGAGAGAGAGAG 1224
 DB 1081 GAGATATCTT-----TCGAGATATTTTCCCGCTGGGTGAGAGAGAGAGAGAGAG 1131
 QY 1225 GACTTCAAAAG 1284
 DB 1132 GACTTCAAAAG 1191
 QY 1285 CGTAAATTAATTTTGGCAATACCGATATATTAATTAATTAATTAATTAATTAATTA 1344
 DB 1192 CGTAAATTAATTTTGGCAATACCGATATATTAATTAATTAATTAATTAATTAATTA 1248
 QY 1345 ATGCAACCGTTTGGGTATTTCAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1404
 DB 1249 AACTGATAG 1308
 QY 1405 CCGAACAACCTAATATCTTCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1461
 DB 1309 AGGATAG 1368
 QY 1462 ATTGAATCTGTTTACAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1521
 DB 1369 ATTGAATCTGTTTACAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1422
 QY 1522 CATGATTTATCAATGAG 1581
 DB 1423 CATGATTTATCAATGAG 1482
 QY 1582 TCGACACATCAAGATAG 1641
 DB 1483 TCGACACATCAAGATAG 1542
 QY 1642 CTGCACTAATAAGATTTTGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1701

DB 1543 CCGCGGTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1602
 QY 1702 GCTGGGCT 1710
 DB 1603 AAAGCACT 1611

RESULT 9
 AB161456
 LOCUS
 DEFINITION
 Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2 genes for putative mosquitocidal toxin and hypothetical protein, complete cds.
 AB161456 3931 bp DNA linear BCT 03-FEB-2004
 AB161456
 AB161456 GI:41688282

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL

Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan (E-mail: ikeya@nab.agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex.2487), Fax: 81-011-706-2487)

Location/Qualifiers
 1. .3931
 /organism="Bacillus thuringiensis serovar entomocidus"
 /mol_type="genomic DNA"
 /strain="INA288"
 /serovar="entomocidus"
 /db_xref="taxon:1436"
 1. .2061
 /gene="cry4Ba like"
 1. .2061
 /gene="cry4Ba like"
 /codon_start=1
 /transl_table=11
 /product="putative mosquitocidal toxin"
 /protein_id="BAD08532.1"
 /db_xref="GI:41688283"
 /translation="MNSYONKNEYELINAPNSNTNMPNRYFANDPNAMKNGNYKDW LDI CN EYRYSNEA V RNTKAMS FGVGIVSTLIGVIGPISVTLGAILGVTVAVLF NPADRYDNKTETGVILIAIKELIYEIGKEMANAKALDGLIYKMKYNDKLNTPK NGKSPVEONEIORVPADTNNSFLILISQOUGHVSFLPLPAVANFLLLRDVS IYKEMGYNNIIIEGHSQDLMDTODYTNVAVDYKNGLEBAKKIKNSDGLDWFVNO YRDEMTLTVLDVALPPTVDYKPISTKVELREIYTDMINIINPFPMTNPEGGOF AGYVLAOFNSINENALFRBPHLFTMLKEVGYEFAOYGOSFMTGIONTSYRTVDEP FSGPLGVAVAGGTARSVUNNGDVSYSTWPEPLRNHVEHRLRGCTAYRQVKGHR HDATDRTNSSSKILIGBDSKTRIALTGSRYSFISEIPIYDKETNETIRPPEKYNHL SYISAVATDCGRISGVRGDCFPQMCMTWHSADPVYTHPDKITQISAVAFYIW DTGEGGVSGPFTGDLVYL PYNARILKRLKPTSKYRVAVRYASMGAATLRAEK WSPYGVSFNSFAVEYGDNSKFNFKYLETILSFSFISGVEIILIONLSQILVDKLE FIP1"

2306. .3931
 /note="ORF2"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="BAD08533.1"
 /db_xref="GI:41688284"
 /translation="MFTSGAKNMLKLETTDYREIDOVANSIENNSDSHSGOKRMWDE VHAKLISGRNLLQNGDFEDLPFGMTTSHNHSIQADNSTPKGNITLMGARDIYGTI

CDS

PPYIYOKIDESKLEPYRRLVAFGVSSKDELVVMRYKEIDITIMVNDIPYVPS
MPVCELYDGEOPYRSGKNGVYNSMPVASPSTSPAGCCOMPGKOVCHDSHQEFH
IDGVEDVNTNIGIWLFPKISSPDGYATT.DNLEVEIRGEGEALAVYVCKKRNKO
MEKREMETQADYDRAKQADALFTGSELIHNTLSQIKRANQIVOSIPYVHBMLEPV
PKNRIDLYOELNTRIMQARLYDARNVITNGDTQLOQMHAEGKVEVQOMGTAVLV
LSNWSGVSQNLVHQRHCGVYLVSARKGPGKGYVTMMGCKNGKDETLTFTSCDGYM
TKVEVFPESERVRIEIGETESFYIESIELIMNGSYTSNNQSNMNMDOVSQNSYS
QNTSMYNNNYEAGACTCNQYNNNGCTCNQ"

ORIGIN

Query Match 10.0%; Score 214; DB 1; Length 3931;

Best Local Similarity 69.0%; Pred. No. 7.1e-30;

Matches 330; Conservative 0; Mismatches 130; Indels 18; Gaps 2;

QY 1564 AGAGTAAAGTATTTGGTGGACACATACAGTATGAAAAAGATATGCAATTTATCCCA 1623
DB 1594 ACACCTCAAGTGTGTGGACACATGTAAGCGGATCCGTATATACATTTCCCA 1653
QY 1624 GATTAATTAAGCAAAATTCCTGCAGTAAAGCTTTTCCCTACACAGGATACAGATAT 1683
DB 1654 GATTAATTAAGCAAAATTTCTGCGTGAAAGCCTTTATATAGGATAC-----T 1704
QY 1684 GCAGAGGTTACGTACAGCTGGGCTGTGTTATACAGAGAGATGTATACCTTACCT 1743
DB 1705 GGGGAAGTCAAGTCTCTCTGACCTGTGTTTACAGAGCGCATTTAGTAAAGTTACCT 1764
QY 1744 TATCAAGCAAGTTTAAATATAGCTTTTACCTTGCACCCGAGATATAAATTCAGTGT 1803
DB 1765 TATTAAGCAGTTTGAATAACGTTTAAACCTTACATTCACAGATATAAATTCAGTGT 1824
QY 1804 AGACTTCGCTACGCGAGTGGAGACCTGTCCGTTCCGATAGAAAAGATGTCGCCAAGT 1863
DB 1825 AGAGTTCGCTATGCAAGTATAGGAGCTGTACATTACAGACAGAAAATGTGCGCGTAT 1884
QY 1864 TCTGTTCAATGCTAATTTTCTCGTCAAGCTACAGGTGCTATAGTTCAATTGAT--- 1920
DB 1885 GGATGATATTTCTTATTTTGGATGATATACGGGTGATTCGATTAATTAATTAAT 1944
QY 1921 -----TATGTGACACCTTATGATTAATCAATCAATCAGGTGTAATTAATTA 1974
DB 1945 TTTAAATATTTAGAACTTTATCTGAATCAATTAATATATCTGTTGTAATAATTA 2004
QY 1975 CAAATCTATCTGTTACACACCTTATTTGACAAAGTCAATTTTCCCAATTGACA 2032
DB 2005 CAAACCTATCTTCTTGCGAACTTATGTTGACAAACTTGATTTATACCAATTTAA 2062

RESULT 10
BTU88189 2028 bp DNA linear BCT 01-OCT-1998
LOCUS Bacillus thuringiensis jegathesan insecticidal protein Jegt74 gene,
DEFINITION complete cds.
ACCESSION U88189.1 GI:3668334
VERSION U88189.1
KEYWORDS
SOURCE Bacillus thuringiensis serovar jegathesan
ORGANISM Bacillus thuringiensis serovar jegathesan
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
cereus group.
1 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Isolation and characterization of insecticidal genes from Bacillus
thuringiensis subsp. jegathesan
Unpublished
2 (bases 1 to 2028)
Kawalek, M.D. and Gill, S.S.
Direct Submission
Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
FEATURES
source
1..2028
Location/Qualifiers
/organism="Bacillus thuringiensis serovar jegathesan"
/mol_type="genomic DNA"

/sub_specie="jegathesan"
/db_xref="taxon:56955"
1..2028
/codon_start=1
/transl_table=11
/product="insecticidal protein Jegt74"
/protein_id="AAC61892.1"
/db_xref="GI:3668335"

CDS

ORIGIN
Query Match 9.2%; Score 197.2; DB 1; Length 2028;
Best Local Similarity 54.6%; Pred. No. 1.2e-26;
Matches 524; Conservative 0; Mismatches 398; Indels 38; Gaps 5;

QY 136 ATGAATTCCTTATCAAAATACAAATGATATGAAATTCGTGATGTTCCCGCAATAACCA 195
DB 1 ATGAATTCCTTATCAAAATGAAATGTAATGTAATTAATGATTCATGTAATTAACATA 60
QY 196 AATATGTCMAAGATATCTTTTCCAAAGATCCCAAT-----ATAATTTCC 242
DB 61 AATATGCCAAGATACCTTTTCCGATATGATTCAAATGCTGTGATGAAAAATGGGAAT 120
QY 243 TATTAACCTGACGCTTGTCAGGAAGCCATGCGAAGATACGTGGAAATCACTCCGCA 302
DB 121 TATTAAGATGTTGAATGAATGATGATGATTAATCTCTTATTTTGGAAACACTTGA 180
QY 303 TATTAAGATATGGAACATACCTTATCAATCTTCTGTAGAAACCCGGATATGGTGAAT 362
DB 181 GTTTCAGCAAGTATTTTCTTCTATTAATCTTGACAGATCTTCCATAGAGAGC 240
QY 363 TCCGTATATTTTCAATATTAACAACTCATCCGTTCTTGTCATCTGTGGCAGC 422
DB 241 GCATTTGCTTGTAGTATCTTATGAGAGATTTGGCCGAGACAGAAAGCTCGTTCC-C 299
QY 423 ACTTCTATATGTGATTAGTATCTAATTTGTAAGAGTACAGAGAGCGTGTAAAG 482
DB 300 TTTGTCGTAGCGGATGTAATCGTTTATTCGTAAAGCGCTTGACCAAAACGCTATTA 359
QY 483 TGACGGGTTGCAAGTTTGAAGGTGAATGACCTTATCAAGATTAATTAATCTTCATTA 542
DB 360 CAGGGCAACGGGAAATTTAACGGTTTAAATGACATATTAACGGTATTAATTA 419
QY 543 TCTTGAGATTTGGCTTACAGATTAATCAATCTTAAAAAATCTTGCTGA-----CGTAG 595
DB 420 TCTCCAAAGTTGTATGATCTGCAATTCCTCGAATCCTCAGGGGATTTGCCAGCTTGA 479
QY 596 TTAACAGTTTCAAGACG-----GGAAGAGATTTCACTAACTTTAGCAGG 644
DB 480 AGAAGACAGTAAAGAAAGCTTGAAGAGATTAAGAGGATTTAGAAAGGACCTAGCAG 539
QY 645 GTCATTAATCAAGACGAAGCTGAATATTAATTTGCTAGGTATGTCAGAGCTGCAAA 704
DB 540 TGAATTTGCAAGCGGTAGTCAATATATTAATTAATTTATTTAGCAAGCTGCAAA 599
QY 705 TGTGATTTATTAATTAAGGAGCGAGTAAATTAATAAAGATGGGACTAGTGTG 764
DB 600 TATTAATTTATGATTAATTAAGAGCTATGCAATTTAGAAAGATTTGGGTTAATAG 659
QY 765 TCCACCGTTGATTCAGGGTCAAGGAAGCTGA-----TTGTAAAGACGGTTAAAGC 818
DB 660 ACCTGAGGTGATACCTATTAATTAATGTCGAAAGATCTTTTGAAGGAAATTTTAAT 719

AUTHORS Bosch, H. Jan. and Stiekema, W. Johannes.
 TITLE Hybrid toxin
 JOURNAL Patent: US 6204246-A 9 20-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..3468
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 8.0%; Score 172.4; DB 6; Length 3468;
 Best Local Similarity 54.2%; Pred. No. 4,2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGATATAGTAACTATTGGACATACCTTATATACATTTCTGCTAGAAC 346
 DB 158 GCGATGACAGAAAAGACAGATATCTATTGGACAACCAATAGCTCTTATACAGCAC 217
 QY 347 CCGGATAGTGGAAATTCCTGTAATTTT-----CAATATAACAACATCATTCCT 400
 DB 218 CTTCCTTACTGATTAATTTCAATAGTATGACCTTATAGGTAAGTCTAGAGAGTA 277
 QY 401 CTTCGTCATCTGTCGACGACCTTCTATATGTATTTAGTATCTATATATTCGTAAG 460
 DB 278 GTAGTGAACAATCATTACATGATTTGTATATGTGACTTATATCTATATGATTAC 337
 QY 461 AGGTAGACGAGACGCTTTAAGTACGCGGGTTCAGATTTTGGAGGTAATGACTGCTT 520
 DB 338 GGGTAAAGTACAGTGTTTAAATGATGGATTCAGATTTTAAATGGTTCGTACTTAT 397
 QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565
 DB 398 ACAGAACTATTTAGAGCTCTGATAGCTGGAATAGAAATCCTAATTCGCTTCGCTG 457
 QY 566 AATCAATCCTAATAAACTTGTCAGCTAGTAACTCAAGTCCAAAGCAGGGAAGAGAT 625
 DB 458 AAGAACTCGTACTCGTTTGAATGCGACATCAGATTTGATAGATTTTAAACCCGAG 517
 QY 626 TCACTAACTTTTACGAGGTCATTATCAAGACAGAAAGCTGAAATTTATTTAGCTTA 685
 DB 518 GGTCTTTAAGAAATGGTGGCTCGTTAGCTAGACAAATGCCCATAATTTATTTACCTT 577
 QY 686 CGTATGCAAGCTGCAATGTGCTATTATTAATAGGACGCAAGTTAAATATPAAAA 745
 DB 578 CTTTTGACGACCTGCAATTTTCCATTATTAATTAAGATGCTAATGATATATGGCA 637
 QY 746 AAGAAATGGGAGCTAGTGTGCCACCGTTATCCAGGGTCAGGGAACAGATTGTAAAG 805
 DB 638 CTAAATGGGGGCTATACATGCTACACCTTTATA-----ATTATCAAT 682
 QY 806 AGCGTTTAAAGCGAAATTAAGAGATATCTAATTTGTGAGGGTGTATACAGAG 865
 DB 683 CAAAATAGTAGAGCTTATGAATATATCTGATTAATGCGTACATGATGATATATCGAG 742
 QY 866 GTTAAATCAGATTAAGACAGCGGGTTCAGATGCTGAAGTTTGGTCAAAATTAATAAT 925
 DB 743 GTTTCACGAACTAAGCAACGAGGCACTAGTGTCTAGAGCTTGGTTAGAAATTTCAATAGAT 802
 QY 926 TTGCTAGAAATGAGCTGGCGGTATTTGATATTTATTTGCTATATTTCAACTATAGAT 985
 DB 803 ATGTGAGAGATGACATTTATGATGATTAATAGTAGACATCAATTTCAAGCTTGATA 862
 QY 986 TTGAAAATATCCATTAGCAACAGTGTAGAGTTAATCAGGAAATTTATACAGATCCAG 1045
 DB 863 TTACTATATCCCAATAGAAACAGATTTTCAGTTGATAGGTCATTTTATACAGATCCAA 922
 QY 1046 TGGGATATTACGGGGGAAATTAAGTTGGGA 1077
 DB 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 13
 AR567184 3468 bp mRNA linear PAT 08-OCT-2004
 LOCUS AR567184

DEFINITION Sequence 9 from patent US 6780408.
 ACCESSION AR567184
 VERSION AR567184.1 GI:53984827
 KEYWORDS
 SOURCE
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 3468)
 AUTHORS Bosch, H. J. and Stiekema, W. J.
 TITLE Genes encoding hybrid bacillus thuringiensis toxins
 JOURNAL Patent: US 6780408-A 9 24-OCT-2004;
 SynGenea Participations AG; Schwarzwaldallee;
 GBX;

FEATURES

source

1..3468
 /organism="unknown"
 /mol_type="mRNA"

ORIGIN

Query Match 8.0%; Score 172.4; DB 6; Length 3468;
 Best Local Similarity 54.2%; Pred. No. 4,2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGAAATCAGTCTCGATATAGTAACTATTGGACATACCTTATATACATTTCTGCTAGAAC 346
 DB 158 GCGATGACAGAAAAGACAGATATCTATTGGACAACCAATAGCTCTTATACAGCAC 217
 QY 347 CCGGATAGTGGAAATTCCTGTAATTTT-----CAATATAACAACATCATTCCT 400
 DB 218 CTTCCTTACTGATTAATTTCAATAGTATGACCTTATAGGTAAGTCTAGAGAGTA 277
 QY 401 CTTCGTCATCTGTCGACGACCTTCTATATGTATTTAGTATCTATATATTCGTAAG 460
 DB 278 GTAGTGAACAATCATTACATGATTTGTATATGTGACTTATATCTATATGATTAC 337
 QY 461 AGGTAGACGAGACGCTTTAAGTACGCGGGTTCAGATTTTGAAGGTAATGACTGCTT 520
 DB 338 GGGTAAAGTACAGTGTTTAAATGATGGATTCAGATTTTAAATGGTTCGTACTTAT 397
 QY 521 ATCAAGATTATATCTTC-----ATTATCTTGAGATTGGCTTACAGATA 565
 DB 398 ACAGAACTATTTAGAGCTCTGATAGCTGGAATAGAAATCCTAATTCGCTTCGCTG 457
 QY 566 AATCAATCCTAATAAACTTGTCAGCTAGTAACTCAAGTCCAAAGCAGGGAAGAGAT 625
 DB 458 AAGAACTCGTACTCGTTTGAATGCGACATCAGATTTGATAGATTTTAAACCCGAG 517
 QY 626 TCACTAACTTTTACGAGGTCATTATCAAGACAGAAAGCTGAAATTTATTTAGCTTA 685
 DB 518 GGTCTTTAAGAAATGGTGGCTCGTTAGCTAGACAAATGCCCAATATTTATTTACCTT 577
 QY 686 CGTATGCAAGCTGCAATGTGCTATTATTAATAGGACGCAAGTTAAATATPAAAA 745
 DB 578 CTTTTGACGACCTGCAATTTTCCATTATTAATTAAGATGCTAATGATATATGGCA 637
 QY 746 AAGAAATGGGAGCTAGTGTGCCACCGTTATCCAGGGTCAGGGAACAGATTGTAAAG 805
 DB 638 CTAAATGGGGGCTATACATGCTACACCTTTATA-----ATTATCAAT 682
 QY 806 AGCGTTTAAAGCGAAATTAAGAGATATCTAATTTGTGAGGGTGTATACAGAG 865
 DB 683 CAAAATAGTAGAGCTTATGAATATATAGATTAATGCGTACATGATGATATATCGAG 742
 QY 866 GTTAAATCAGATTAAGACAGCGGGTTCAGATGCTGAAGTTTGGTCAAAATTAATAAT 925
 DB 743 GTTTCACGAACTAAGCAACGAGGCACTAGTGTCTAGAGCTTGGTTAGAAATTTCAATAGAT 802
 QY 926 TTGCTAGAAATGAGCTGGCGGTATTTGATATTTATTTGCTATATTTCAACTATAGAT 985
 DB 803 ATGTGAGAGATGACATTTATGATGATTAATAGTAGACATCAATTTCAAGCTTGATA 862
 QY 986 TTGAAAATATCCATTAGCAACAGTGTAGAGTTAATCAGGAAATTTATACAGATCCAG 1045

Db 863 TTACTATTACCAATAGAAACAGATTTCAGTGTAGAGGTCATTATACAGATCCA 922

QY 1046 TGGATATTACAGGGGAAATTAGTTGGGAA 1077

Db 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 14

BD062618 3471 bp DNA linear PAT 27-AUG-2002

LOCUS Toxins active against pests.

DEFINITION BD062618

ACCESSION BD062618.1 GI:22608221

VERSION JP 2001507208-A/42.

KEYWORDS JP 2001507208-A/42.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3471)

AUTHORS Schenpf,E.H., Wicker,C., Narva,K.E., Walz,M. and Stockhoff,B.A.

TITLE Toxins active against pests

JOURNAL Patent: JP 2001507208-A 42 05-JUN-2001;

MYCOGEN CORP

COMMENT PN JP 2001507208-A/42

PD 05-JUN-2001

PI ERNEST H SCHENPF,CAROL WICKER,KENNETH E NARVA,MICHELE WALZ, PI BRIAN A STOCKHOF

PC C12N15/32,C12N1/68,C12N15/82,C07K14/325,A01N63/00,A01H5/00 CC Strandedness: Single;

CC Topology: linear;

FF Key Location/Qualifiers.

FEATURES

source 1..3471

Location/Qualifiers

1..3471

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 8.0%; Score 172.4; DB 6; Length 3471;

Best Local Similarity 54.2%; Pred. No. 4.2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATCAGTCTCGATATAGTAACTATTTGGGACATCTTAATTCATTCTGTGTAAC 346

Db 158 GCGATGACGAGAAAGACGATCTATTTGGGACACATAGTCTCTTATACACAC 217

QY 347 CCGGTATAGGTGAATTCCTGTATATTTT-----CAATATAACAACTCATTCGGT 400

Db 218 CTCTCTTACTGCGATTATTTCAATAGTATGTACCTTAATAGTAAGTAAGTACAGAGTA 277

QY 401 CTCTGTCATCTGTGGGACACTTCTTATATGTATTTAGTATCTATATTCGTAAAG 460

Db 278 GTAGTGAACATTCATATCAGATTGTCTATATGTATTTATTTATTTATTTAGATTAC 337

QY 461 AGGTAGACGAGCGGTGTATAGTACCGGGTGCAGATTTTGAAGGTGAATGACTCTT 520

Db 338 GCGTAATCAGAGCTTTTAAATGATGAGATGCAATTTTAAATGTTCTGTACTCTTAT 397

QY 521 ATCAAGTATATATCTTC-----ATTATCTTGAAGATTGCTTACAGATA 565

Db 398 ACAGGAATCTTTAGAGGCTCTGTAGTACGTGAATTAAGAAATCTTAATTCGTCTGCTG 457

QY 566 AATCAATCTTAATAAACTGTGTCGACGTGAAGTTAAAGCTTCCAGACGCGGAAGAAAT 625

Db 458 AAGAACTCCGTACTCGTTTGAATCGCCGACCTGAGATTGTAGATTTTAAACCGAG 517

QY 626 TCACTAACTTTTGAAGGTCATTATCAAGACGAAAGCTGAATATTTATTTGCTTA 685

Db 518 GGTCTTTTAAAGAAATGGGCTCGTTAGTACGAAAAATGCCAAATTTATTTATCTT 577

QY 686 CGTATGTGCAAGCTGCAAAATGTGATTATTTACTATTAAAGGACGCGATTAAATATAAA 745

Db 578 CTTTGGACGCGTGCATTTTTCATTATTTACTACTAAGGAGTCTACTAGATATGCA 637

QY 746 AAGATGGGAGCTAGTGTGTCCACCGTTGATCAGGGGTGAGGAGAACTGATTGTAAG 805

Db 638 CTAAATGGGGCTATCAATGCTACACTTTTATA-----ATTATCAAT 682

QY 806 AGCGTTTAAAGCGAAATTAAGAGTATCTAATTTGTGTAGGGGTGATTAACAAG 865

Db 683 CAAACTAGTAGAGCTTATGAACTATATCTGATTATTGCGTACATTTGTTATATGAG 742

QY 866 GTTATAGTCAATTAACAGCGCGGTACAGTCTGAAGTTTGTGCAATTTATTAAT 925

Db 743 GTTCAACGAACTAAGACGAGGACGAGGCTAGTCTCAGCTTGTGTTAAGATTCATGAT 802

QY 926 TTGCTAGAGAAATGAGCTTGGCGGTATTTGATATTTATTTGCTATATTTCCAACTTATGAT 985

Db 803 ATCTTAGAGAGATGACCTTATGATGTATTTAGATATAGTACATCATTTTCAAGCTTGATA 862

QY 986 TTGAAAAATATCCATTAGCAACAAGTGTAGATTAACTAGGAAATTTATACAGATCCAG 1045

Db 863 TTACTATTACCAATAGAAAGATTTTCAGTTGAGTAGGTCATTATACAGATCCA 922

QY 1046 TGGATATTACAGGGGAAATTAGTTGGGAA 1077

Db 923 TTGGTTTGTACATCGTAGTAGTCTTAGGGGA 954

RESULT 15

BD128371 3471 bp DNA linear PAT 18-SEP-2002

LOCUS Toxin active on Oestrinlanubialis.

DEFINITION BD128371

ACCESSION BD128371.1 GI:23223316

VERSION JP 2002500166-A/42.

KEYWORDS unidentifed

SOURCE unidentifed

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 3471)

AUTHORS Schenpf,E.H., Wicker,C., Narva,K.E., Walz,M., Stockhoff,B.A. and

TITLE Cohn,J.M.

JOURNAL Toxin active on Oestrinlanubialis

Patent: JP 2002500166-A 42 08-JAN-2002;

MYCOGEN CORP

COMMENT OS Unidentifed

PN JP 2002500166-A/42

PD 08-JAN-2002 JP 2000526647

PF 15-DEC-1998 JP 2000526647

PI ERNEST H SCHENPF,CAROL WICKER,KENNETH E NARVA,MICHELE WALZ, PI BRIAN A STOCKHOF,JUDY MULLER COHN

PC A01N63/02//C07K14/325,C12N15/09,C12N15/00

CC Strandedness: Single;

CC Topology: linear;

CC Toxin active on Oestrinlanubialis

FF Key Location/Qualifiers

FF source 1..3471

Location/Qualifiers

1..3471

/organism="unidentifed"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 8.0%; Score 172.4; DB 6; Length 3471;

Best Local Similarity 54.2%; Pred. No. 4.2e-22;

Matches 440; Conservative 0; Mismatches 336; Indels 36; Gaps 3;

QY 287 GGGATCAGTCTCGATATAGTAACTATTTGGGACATCTTAATTCATTCTGTGTAAC 346

Db 158 GCGATGACGAGAAAGACGATCTATTTGGGACACATAGTCTCTTATACAGCAC 217

OY	347	CCGGATATGGGGAATTCCTGTAATATTT-----CAATAATAACAACACTCATTCGGT	400
Db	218	CTTCTCTTACTGGATTAAATTCAATAGTAATATGACTTTATAGTAACTACTACGAGGTA	277
OY	401	CTTCTGTCATCTGTGGCAGCACTTCTGATATGATATTGATATCTAATTGGTAAAG	460
Db	278	GTAGGGAGCAATCCATATCAGATTGTCTATATGTGACTTATATCTATTTATGATTTAC	337
OY	461	AGGTAGACGAGAGCGCTGTTAAATGACGAGGCTTGACAGATTTTGAGGGTGAATGACTGCTT	520
Db	338	GGGTAGACTCAGAGTGTTTTAAATGATGAGGATGTGCAGATTTTAAATGTTCTGTACTCTTAT	397
OY	521	ATCAAGATTAATATCTC-----ATTATCTGAGGATTCGCTTACAGATA	565
Db	398	ACAGGACTATTTTAGAGGCTCTGTGATAGCTGGAATAAATCTTAATTCCTCTTGCTG	457
OY	566	AATCAAAATCTTAAAAAACCTGTGACGTAGTAAACAGTTCACAGCAGCGAAGAGAT	625
Db	458	AAGAATCTCGTACTGTTTGAATGCGCACTCAGATTTTGATGAAATTTTAACCCAG	517
OY	626	TCACTAAACCTTTAGCAGGGTCATTATCAAGCAGAAAGCTGAATATTTATTTTGCTTA	685
Db	518	GATCTTTAACGAATGATGGCTGCTGTAGCTAGCAAAAAGCCCAATATTTATTTACCTT	577
OY	686	CGTATGTCAGCTGCTCAATGTCATTTATTACTTATTAAGGAGCGCACTTAAATTAATAA	745
Db	578	CTTTTGCGAGGCTGCTGATTTTTCATTTATTACTTAAGGAGTCTATGATATGGCA	637
OY	746	AAGATGGGGACTAGTGTGTCCACCGTTGATCCAGGGTCAAGGAGAACTGATTTGTAAAG	805
Db	638	CTAATTTGGGGGCTATACAAATGCTACACCTTTATATA-----ATTATCAAT	682
OY	806	AGCGTTAAAGCGAAAATMAAAGATATCTAATTAATTGTGTAGGGTGTATTAACAAG	865
Db	683	CAAAACTAGTAGGCTTATGTAACATATATACGATTATTTGCGTACATTTGTATATCAG	742
OY	866	GTTTATGATCAATTAAGACAGGCGGGTACAAGTGTGCAAGTTTGGTCGAAATTTAATTAAT	925
Db	743	GTTTCAGGAACCTAAGACACAGAGGCACTTAGTGCTACAGCTTGGTTAGAAATTTCAAT	802
OY	926	TTTCGTAGAGAAATGACGTTGGCGGATTTGGAATATTAATTTGCTAATTTTCCACTATGAT	985
Db	803	ATCGTAGAGATGACATTTGATGTATTAGTATATGTAACATCAATTTCCAGTCTTGATA	862
OY	986	TTGAAAAATATCCATTAGCAACAGGTGATAGCTTACTAGGGAATTTTATACAGATCCAG	1045
Db	863	TTACTAATTAACCATATGAAACAGATTTTCAGTTGATGATAGGGTCAATTTATACAGATCAA	922
OY	1046	TGGGATATTCAGGGGGAATTAATGTTGGGA	1077
Db	923	TTGGTTTGTACATGCTAGTATGCTCTTAAGGGA	954

Search completed: December 19, 2005, 09:48:28
Job time : 7241.94 secs